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ABB93248 AAG28589 AAG28588 AAG28587

AAG40137 AAG40136

Maize caffeic come Arabidopsis thalia Arabidopsis thalia

AAG25274 AAG25598

AAY43041 AAG31304

AAG25597 AAG47427

AAG25596 AAG47426 AAR34764

ABB93811

AAR63203 AAE12021 AAG25275

AAG31305

AAY01133 AAU80015 AAW84132 AAR34763

pPLC4 translation Aspen bispecific O 5-hydroxyconiferal Exemplery caffeic OWTI.A and OWTI.B Rice caffeic acid An (iso) eugenol m Arabidopsis thalia

Soybean caffeic ac Clarkia breweri IE

AAE16510 AAE29785

AAE16516 AAW84128 ALIGNMENTS

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WO200037656-A2
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New polynucleotide encoding flavonoid biosynthetic enzymes for creating transgenic plants and for immunological screening of cDNA libraries
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AAY96584 standard, Protein; 358
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                         AAY96583-87 are (partial) isoflavone O-methyltransferases isolated from various soybean (Glycine max) tissues. CDNA libraries set, srl, strlc and ssllc were prepared from soybean embryo (19 days after flowering), root, 8-day old root and seed (25 days after flowering).

Isoflavone O-methyltransferase catalyses the first step in degradation of daidcain. Suppression of this enzyme will yield higher concentrations of this beneficial isoflavone in. e.g. soybean seed. Ravonoids serve as co-pigments in flower colour, stimulate pollen tube growth, attract pollenators, act as feeding deterrents and protect against UV isradiation in fruits and seeds. The cDNA and proteins can be used to isolate homologues, for immunological screening and for positive
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Flavonoid; flower colour; growth; pollination; irradiation.
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100.0%; Pred. No. 2.9e-189;
ive 0; Mismatches 0;
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           Claim 10; Page 32-33; 39pp; English.
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Best Local Similarity 100.
Matches 358; Conservative
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AAY96583-87 are (partial) isoflavone O-methyltransferases isolated from various soybean (Glycine max) tissues. CDNA libraries set, srl, srrlc and sell were prepared from soybean embryo (19 days after flowering), root, 8-day old root and seed (25 days after flowering).

Isoflavone O-methyltransferase catalyses the first step in degradation of dialdzein. Suppression of this enzyme will yield higher concentrations of this beneficial isoflavone in, e.g. soybean seed. Plavonoids serve as co-pigments in flower colour, stimulate pollen tube growth, attract pollenators, act as feeding deterrents and protect against UV irradiation in fruits and seeds. The cDNA and proteins can be used to selection methods.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 YFLEPNCQGAMNQLKRWVHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSOMLN 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGDMFNSIPQADAVLLKWVLHNWTDENCIKILQKCRDSISSKGNSGKVIIIDAVINBKLD 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57
                                                                                                                                                                                                       New polynucleotide encoding flavonoid biosynthetic enzymes for creating transgenic plants and for immunological screening of cDNA libraries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
8
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                                                                Falco SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84; Indels
                                                                Fader GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycine max isoflavone O-methyltransferase.
(DUPO ) DU PONT DE NEMOURS & CO E I.
                                                             odell JT,
                                                                                                                                                                                                                                                                                            Claim 10; Page 37-39; 39pp; English
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Best Local Similarity 54.94
Matches 196; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                       Famodu OO, McGonigle B,
                                                                                                                    2000-442680/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         350 AA;
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ņ,

O-methyltransferase; soybean; degradation; daidzein; flower colour; growth; pollination; irradiation.

(first entry)

SC;

Falco

Fader GM,

McGonigle B,

Ξ. odell JT,

99WO-US30338 98US-0113190

m

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New polynucleotide encoding flavonoid biosynthetic enzymes for creating transgenic plants and for immunological screening of cDNA libraries
                                Glycine max partial isoflavone O-methyltransferase.
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                                                                                                                                                                                                                                                                      WPI; 2000-442680/38
                                                                                                                                                                                                                                                                                  N-PSDB; AAA29324
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                                                                                                                                                                       20-DEC-1999;
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       26-SEP-2000
                                                                                               Slycine max.
                                                                                                                                               29-JUN-2000
                                                         Isoflavone
Flavonoid;
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Isoflavone O-methyltransferase catalyses the first step in degradation of daidzein. Suppression of this enzyme will yield higher concentrations of this beneficial isoflavone in, e.g. soybean seed. Flavonoids serve as co-pigments in flower colour, stimulate pollen tube growth, attract pollentenses, act as feeding deterrents and protect against UV irradiation in fruits and seeds. The cDNA and proteins can be used to insolate homologues, for immunological screening and for positive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAFRDCNWVFBGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFV 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 351;
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                                                                                                                                                                   Falco
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               /note= "Encoded by GAAGATCATGAA"
                                                                                                                                                                   Fader GM,
                                                                                                                                                                McGonigle B, Odell JT,
                                                                                                                                       (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                Claim 10; Page 34-35; 39pp; English.
                                                                                        99WO-US30338.
                                                                                                                98US-0113190.
                                                                                                                                                                                        WPI; 2000-442680/38
Misc-difference 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                         351 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                  selection methods.
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                                     WO200037656-A2
                                                                                       20-DEC-1999;
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                                                              29-JUN-2000
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AAY96583-87 are (partial) isoflavone O-methyltransferases isolated from various soybean (Glycine max) tissues. CDNA libraries se4, sr1, srrlc and sellc were prepared from soybean embryo (19 days after flowering), root, 9 day old root and seed (25 days after flowering).

Isoflavone O-methyltransferase catalyses the first step in of daidzein. Suppression of this enzyme will yield higher concentrations of this beneficial isoflavone in, e.g. soybean seed. Flavonoids serve as co-pigments in flower colour, stimulate pollen tube growth, attract pollentucis, act as feeding deterrents and protect against UV irradiation in fruits and seeds. The CDNA and proteins can be used to isolate homologues, for immunological screening and for positive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CQGAWNQLKRWVHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDC 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 SKAGFVQQFMRFLAHDGIFDIRESQDDHELAYALTPASKLLVSCSDHCLSPMVRMNTDPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 LWTTYHHFGEWIRGEDPTVHBTAFGTSFWGLLEKNPTOMSLFNEAMASDSRAVDLALKNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 TSVFEGLDSMVDVGGGTGTTARIICEAFPKLKCVVLDLPHVVSNLTGTNNLSFVGGDMFN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299 TKLSLDIVMS-TWNGRERSEKEWKQMFIEAGFQHCKIFPIFGFRSLIELYP 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53.3%; Score 1006; DB 21; Length 348; 54.7%; Pred. No. 1e-96; ive 64; Mismatches 91; Indels 4
Claim 10; Page 35-36; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 192; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      selection methods
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AAY96586 standard; Protein; 348

AAY96586 RESULT

AAY96586;

EXXX X

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128 GLSGESGTAFEKALGTNIWGYMAEHPEKNQLFNEAMANDSRLIMSALVKECGNIFNGITT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 MRYLAHNGFFEIVRIHDNIEAYALTAASELLVKSSELSLAPMVEYFLEPNCQGAWNQLKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 MRYLVHMKLFTKASIDGELR-YGLAPPAKYLVKGWDKCMVGSILAITDKDFMAPWHYLKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 IVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QALLYKHLLGFIDSKCLKWWVELDIPDIIHSHSHGQPITFSELVSILQVPPTKTRQVQSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 WVHEBDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAF-RDCNWVFEGLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                257 LKLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDERQVTELKLLMDVHM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents norcoclaurine 6-0-methyltransferase (6-0MT). Also described is a method for the preparation of the secon metabolite of a plant derived from coclaurine or reticuline.
                     TELKLIMDVHMACIINGKERKEEDWKKLFMEAGFQSYKISPFTGYLSLIEIYP 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New norcoclaurine 6-0-methyl-transferase - useful for preparation
                                       TRIKLSLDIVMS-TWNGRERSEKEWKQMFIEAGFKHCKIFPIFGFRSLIELYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 347;
                                                                                                                                                                                                                                                        Coptis japonica; norcoclaurine 6-0-methyltransferase; 6-0MT; secondary metabolite; coclaurine; reticuline.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 33.7%; Score 636.5; DB 20; Length Local Similarity 38.9%; Pred. No. 7.3e-58; es 133; Conservative 70; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  305 MINTGGKERTEEEWKKLIHDAGYKGHKITQITAVQSVIEAYP 346
                                                                                                                                                                                                                            Coptis japonica norcoclaurine 6-0-methyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              317 ACIINGKERKBEDWKKLFMEAGFQSYKISPFTGYLSLIEIYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MITC ) MITSUI PETROCHEM IND CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 11-12; 27pp; Japanese
                                                                                                                                Ä
                                                                                                                                Protein; 347
                                                                                                                                                                                                                                                                                                                                                                                                                            97JP-0355045.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          secondary plant metabolite
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N-PSDB; AAX90136.
                                                                                                                               AAY24396 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 347 AA;
                                                                                                                                                                                                                                                                                                       Coptis japonica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY96583-87 are (partial) isoflavone O-methyltransferases isolated from various soybean (Glycine max) tissues. CDNA libraries se4, sr1, srr1c and self were prepared from soybean embryo (19 days after flowering), root, 8-day old root and seed (25 days after flowering).

Isoflavone O-methyltransferase catalyses the first step in degradation of daidzein. Suppression of this enzyme will yield higher concentrations of this beneficial isoflavone in, e.g. soybean seed. Plavonoids serve as pollenators, act as feeding deterrents and protect against UV irradiation in fruits and seeds. The CDNA and proteins can be used to instant and seeds. The cDNA and proteins can be used to instant in concerning and for positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotide encoding flavonoid biosynthetic enzymes for creating transgenic plants and for immunological screening of cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLLMTTYHHFGEWIRGEDPTVHETAFGTSFWGLLEKNPTQMSLFNEAMASDSRMVDLALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PNCQGAWNQLKRWVHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                           daidzein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.9%; Score 997; DB 21; Length 350; 54.1%; Pred. No. 9e-96; ive 65; Mismatches 93; Indels
                                                                                                                                                      Isoflavone O-methyltransferase; soybean; degradation; daid:
Flavonoid; flower colour; growth; pollination; irradiation
                                                                                                                                                                                                                                                                                                                                                                                             sc;
                                                                                                                                                                                                                                                                                                                                                                                             Falco
                                                                                                                          Glycine max partial isoflavone O-methyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                             Fader GM,
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                                                                                                                                                                                                                                                                                                                                                                                          Odell JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; Page 30-31; 39pp; English.
                                AAY96583 standard; Protein; 350 AA.
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                                                                                                                                                                                                                                                                                                                               98US-0113190
                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                            McGonigle B,
                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-442680/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 191; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         350 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            selection methods
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                                                                                                                                                                                                                                                                                                  20-DEC-1999;
                                                                                           26-SEP-2000
                                                                                                                                                                                                       Glycine max
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                                                              AAY96583;
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RESULT 5
              AAY96583
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128 ATTAPFVSLALQPIAACPHALG-ISAWFRQEQHEPSPYGLAFRQTPTIWEHADD----VNA 183
                                                                                                                             227 NVVENLSGSNNLTFVGGDMFKCIPKADAVLLKLVLHNWNDNDCMKILENCKEAISGESKT 286
                                                                                                                                                                                                                                  244 HVVAGAPSDGNVQFVAGNNFESIPPATAVFLKKTLHDWGDDECVKILKNCKQAISPRDAG 303
                                                                                                                                                                                                                                                                                 287 GKVVVIDTVINENKDERQVTELKLIMDVHMACIINGKERKEEDWKKLFMEAGFQSYKISP 346
                                                                                                                                                                                                                                                                                                             304 GKVIILDVVVGYKÇSNIKHQETQVMFDLYMMA-VNGVERDEQEWKKIFTEAGFKDYKILP 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This represents a polypeptide having the enzymatic activity of (8)-3'-hydroxy-N-methylcoclaurine 4'-O-methyltransferase (4'-OMT). A vector containing the DNA can be used to transform a microbe for the recombinant preparation of the enzyme. The enzyme can be used to prepare a secondary metabolite of a plant derived from reticuline which is useful as a raw
         114 LSLAPMVEYFLEP--NCQGAWNQLKRWVHEEDLTVFEVSLG---TP-FWDFINKDPAYNK 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 SLMRYLAHNGFFEIVRIHDNIEAYALTAASELLVKSSELSLAPMVEYFLEPNCQGAWNQL 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 KAQAHVWKIIYGFADSLVLRCAVELGIVDIIDNNN--QPMALADLASKLPVSDVNCDNLY 70
                                                                                                   168 SFNEAMACDSO-MINIAFRDCNWVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 QGQALLYKHLLGFIDSKCLKWMVELDIPDIHSHSHGQPITFSELVSILQVPPTKTRQVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (8)-3'-hydroxy-N-methylcoclaurine 4'-O-methyltransferase (4'-OMT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (S)-3'-hydroxy-N-methylcoclaurine 4'-O-methyltransferase; 4'-OMT; enzyme; secondary metabolite; reticuline; drug.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New (S)-3'-hydroxy-N-methylcoclaurine 4'-O-methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.8%; Score 580.5; DB 20; Length 34.0%; Pred. No. 5.8e-52; Live 83; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MITC ) MITSUI PETROCHEM IND CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY27183 standard; Protein; 350 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                     363 VIGDVSVIIEVYP 375
                                                                                                                                                                                                                                                                                                                                                                        347 FTGYLS-LIEIYP 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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AAY27183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is a caffeic O-methyltransferase, encoded by a cDNA clone (see AAX25200) isolated from a line A643 cDNA library. The invention provides methods and compositions relating to altering lignin biosynthesis and/or the lignin composition of plants. Isolated nucleic acids (see AAX25196-216) that code for proteins (see AAX05657-77) involved in lignin biosynthesis are claimed. Also claimed are recombinant expression cassettes, host cells (especially maize or sorghum), and transgenic plants and seeds. The claimed nucleic acids can be used to transform a plant to modulate lignin biosynthesis. A claimed method involves transforming a plant cell with a recombinant expression cassette or promoter, growing the plant cell under plant growing conditions, and inducing expression of the polynucleotide for a time sufficient or modulate (preferably increase) lignin biosynthesis in the plant. The plant lignins can be used as a time sufficient material of increased lignin content can be used as a fuel source, immunes the algorithmic content can be used as a fuel source, immunes the algorithmic follows.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 SQDLLQAHDELLHHSLCFAKSLALAVALDLRIPDAIHHHGAG-GATLLQILAETALHPSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 31; Gaps
                                                                                                                                                                                                                             Maize; corn; caffeic O-methyltransferase; lignin; transgenic plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding plant lignin biosynthesis enzymes - used to transform plants to modulate lignin biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 20; Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31.3%; Score 590.5; DB 20; 37.3%; Pred. No. 5.7e-53; ive 62; Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and in the pulp and paper industry. Decree improves the digestibility of fodder crops.
                                                                                                                                                                                                                                                                                                                                                                    /note= "encoded by ACC"
                                                                                                                                                                                                                                                                                                           Location/Qualifiers
227
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                                               AAY05661 standard; Protein; 375 AA
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                                                                                                                                                                                   Maize caffeic O-methyltransferase.
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97US-0057082.
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Best Local Similarity 37,33
Matches 139; Conservative
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N-PSDB; AAX25200.
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                                                                                                                                                                                                                                                                                                                                          Misc-difference
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27-AUG-1997;
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                                                                                         AAY05661,
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RESULT 7
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                                     Sequence
                                                                  Query Match
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                                                                                  Best Loca
Matches
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                                                                               186
                                                                                                                       247 AQAIILKLIHDWNDEDSIKILKQCRNAVPKDG--GKVIIVDVALDEESD-HELSSTRLI 303
                                                                                                                                                                 ADAVLLKLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDERQVTELKLL 311
                                              KRWVHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAF----RDCNWVF 191
                                                                                                        EGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a caffeic O-methyltransferase of maize, encoded by a clone (see AAX25201) isolated from a line A632 library. The invention provides methods and compositions relating to altering lignin biosynthesis and/or the lignin composition of plants. Isolated mucleic acids (see AAX25196-216) that code for plants. Isolated mucleic acids (see AAX25196-216) that code for claimed. Also claimed are recombinant expression cassettes, host calls (especially maize or sorghum), and transgenic plants and calls (especially maize or sorghum), and transgenic plants and calls (especially maize or sorghum), and transgenic plants and calls (especially maize or sorghum), and transgenic plants and calls (especially maize or sorghum), and transgenic plants and calls (especially maize or sorghum), and transgenic plants or modulate lignin biosynthesis. A claimed method involves transforming a plant cell with a recombinant expression cassette comprising a lignin biosynthesis polymucleotide for a time sufficient or modulate (preferably increase) lignin biosynthesis in the plant. The plant lignins can be used as chemical feedstock, plant material of increased lignin content can be used as a fuel source, and in the pulp and paper industry. Decreased lignin content
                                                                  Nucleic acids encoding plant lignin biosynthesis enzymes - used to transform plants to modulate lignin biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maize; corn; caffeic O-methyltransferase; lignin; transgenic plant
                                                                                                                                                                                                                             312 MDVHMACIINGKERKEEDWKKLFMEAGFQSYKISPFTGYLSLIEIYP 358
                                                                                                                                                                                                                                              Claim 9; Page 95-96; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang X;
                                                                                                                                                                                                                                                                                                                                                                                                                      Maize caffeic O-methyltransferase
                                                                                                                                                                                                                                                                                                                                AAX05662 standard; Protein; 370
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                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-AUG-1998;
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27-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                          19-JUL-1999
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                                                                                                                                                                                      61 VSILQVPPTKTRQVQSLMRYLAHNGFFEIVRIH-----DNIEA---YALTAASELLVK- 110
                                                                                                                                                                                                          --SSELSLAPWVEYFLEPNCQG-----AWNQLKR-------WVHEEDLT 145
                                                                                                                                                                                                                                                                                118 EVSTATTLAPFVSLALQPIAASPHALGICAWFRQEQHEPSPYGLAFRQTPTLWEHADDV- 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                      146 VFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQ-MLNLAFRDCNWVFEGLESIVDVGGGT
                                                                                                                                                                                                                                                                                                                                                                                                       217 GGAAAAIAAAFPHVKCSVLDLPHVVAGAPSDGNVQFVAGNMFESIPPATAVFLKKTLHDW
                                                                                                                         1 MASSLNNGRKASEIFQGQALLYKHLLGFIDSKCLKWMVELDIPDIIHSHSGQPITFSEL
                                                                                                                                                                                                                                                                                                                                           --------NALLNKGMVADSRFLMPIVLRQCGEMFRGINSLVDVGGGH
                                                                                                                                                                                                                                                                                                                                                                                                                                      265 NDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDERQVTELKLLMDVHMACIINGKE
                                                                                                                                                                                                                                                                                                                                                                          205 GITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVLLKLVLHNW
                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maize; corn; caffeic O-methyltransferase; lignin; transgenic plant.
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O
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                                                                                             62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a caffeic O-methyltransferase of maize,
                                                               Length 370;
                                                                                             Indels
                                                                                             132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336 RDEQEWKKIFAEAGFKDYKILPVIGDVSVIIEVYP 370
                                                               30.1%; Score 567; DB 20; 34.7%; Pred. No. 1.7e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RKEEDWKKLFMEAGFQSYKISPFTGYLS-LIEIYP 358
improves the digestibility of fodder crops.
                                                                                             64; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 9; Page 96-97; 166pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY05663 standard; Protein; 366 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maize caffeic O-methyltransferase.
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97US-0057082
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                                                                                            Conservative
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                                                                          Local Similarity
les 137; Conserv
                                370 AA;
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99US-0132863.
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99US-0134219.
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99US-0136021.
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990S-0139452.
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990S-0139492.
                              25-FEB-2000; 2000EP-0301439
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99US-0134768
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99US-0135124
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99US-0142390
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25-MAR-1999;
29-MAR-1999;
01-APR-1999;
08-APR-1999;
16-APR-1999;
16-APR-1999;
119-APR-1999;
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04-MAY-1999;
05-MAY-1999;
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18-MAY-1999;
19-MAY-1999;
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25-MAY-1999;
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18-JUN-1999;
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28-APR-1999;
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23-JUN-1999
              11;
concoded by a clone (see AAX25202) isolated from a maize line B73 cDNA library. The invention provides methods and compositions relating to altering lighin biosynthesis and/or the light composition of plants. Isolated nucleic and/or the light code for plants. Isolated nucleic and/or the light biosynthesis are claimed. Also claimed are recombinant expression cassettes, host cells (especially maize or sorghum), and transgenic plants and seeds. The claimed nucleic acids can be used to transform a plant to modulate light biosynthesis. A claimed method involves to modulate light biosynthesis polynucleotide operably linked to a promoter, growing the plant cell under plant growing conditions, and inducing expression of the polynucleotide operably linked to a promoter, growing the plant cell under plant growing conditions, and inducing expression of the polynucleotide for a time sufficient to modulate (preferably increase) light biosynthesis in the plant. The plant lightin content can be used as a fuel source, material of increased light content can be used as a fuel source, and in the pulp and paper industry. Decreased light content canse improves the digestibility of fodder crops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TROVOSIMRYLAHNGFFEIVRIHDNIEA-----YALTAASELLVKSSE----LSLAPM 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 VEYFL-----EPNCQG--AWNQLKR-----------WVREDLTVFEVSLGTPFW 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----NALINKGLLAESRFIMPIVLRECGDEVFRGIDSLVDVGGGHGGAAATIAAA
                                                                                                                                                                                                                                                                                                                                                                                        11 ASBIPQGQALLYKHLLGFIDSKCLKWMVBLDIPDIIHSHSHGQPITFSBLVSILQVPPTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215 FPKLKCWVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVLLKLVLHNWNDNDCMKILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOULLEAHDELFHHCLCRAKSLALAVAQDLRIPDAIHHHGGG--ATLHQILAEAALHPSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 DFINKDPAYNKSFNEAMACDSQ-MLNLAFRDC-NWVFBGLESIVDVGGGTGITAKIICEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                275 NCKEAISGESKIGKVVVIDTVINENKDERQVTELKLIMDVHMACIINGKERKEEDWKKLF
                                                                                                                                                                                                                                                                                                                           28.7%; Score 540.5; DB 20; Length 366;
Llarity 33.3%; Pred. No. 1e-47;
Conservative 70; Mismatches 125; Indels 61;
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IEAGFKDYKIRPVAGLMSVIEVYP 366
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                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 128; Conserv
                                                                                                                                                                                                                                                                                                 Sequence 366 AA;
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0.011-1999; 0.011-1999; 0.011-1999; 0.011-1999; 0.011-1999; 0.011-1999; 0.011-1999; 0.011-1999; 0.011-1999; 0.011-1999; 0.011-1999; 0.011-1999; 0.011-1999; 0.011-1999; 0.011-1999;		- AUG-1999; - AUG-1999;	- AUG-1999; - AUG-1999; - AUG-1999; - AUG-1999; - AUG-1999; - AUG-1999; - SEP-1999; - SEP-1999; - SEP-1999; - SEP-1999; - SEP-1999; - SEP-1999; - SEP-1999; - SEP-1999; - SEP-1999; - SEP-1999;
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990S-0139463-990S-0139463-990S-0139463-990S-0139463-990S-0139463-990S-0139899-990S-0139899-990S-0149899-990S-0140991-990S-0140894-990S-0141335-990S-0144834-990S-0144834-990S-0144834-990S-0144834-990S-0144834-990S-0144834-990S-0144834-990S-0144834-990S-0144834-990S-0144834-990S-0144834-990S-0144834-990S-0144834-990S-0144834-990S-0145918-990S-0145918-990S-0145918-990S-0147335-990S-0145918-990S-0147335-990S-0147335-990S-0147335-990S-0145918-990S-0145918-990S-0147335-990S-0147335-990S-0147335-990S-0147335-990S-0147335-990S-0147335-990S-0147335-990S-0147335-990S-0147335-990S-0149388-990S-0149323-990S-0149323-990S-0149323-990S-0149323-990S-0149323-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-0149923-990S-
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                                                                                                                                                                                                                                                                                                                                                                                       1-JUL-1999;
      Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                             Arabidopsis thaliana protein fragment SEQ ID NO: 49760.
AAG40136 standard; Protein; 382 AA
                                                                                                                                                                                                             99US-0121825.
99US-0123180.
99US-0123788.
99US-0125788.
99US-0126784.
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                                        18-OCT-2000 (first entry)
                                                                                                                          Arabidopsis thaliana
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194 RRVVPRVAGACHGLFDGVTTMVDVGGGTGETMGMLVKEFPWIKGFNFDLPHVIEVAEVLD 253
                                                                                                     312 GENKKTMIVDERDEKLEHVRLMLDMYMMAHTSTGKERTLKEWDFVLKEAGFARYEVRDID 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVPPTKTRQVQSLMRYLAHNGFFEIVRIHDNI-EAYALTAASE--LLVKSSELSLAPMVE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                 297 NENK-----DER--QVTELKLIMD-VHWACIINGKERKEEDWKKLFMEAGFQSYKISPFT
                                              NLTFVGGDMFKCI PKADAVLLKLVLHNWNDNDCMKI LENCKEAI SGESKTGKVVVI DTVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 NNGRKA-SEIFQGQALLYKHLLGFIDSKCLKWMVELDIPDIIHSHSHGQPITFSELVSIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; SEQ ID NO 2459; 261pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.1%; Pred. No. 2.88-30,
tive 70; Mismatches 151; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.9%; Score 527; DB 23; 34.1%; Pred. No. 2.8e-46;
                                                                                                                                                                                                                                                                                                                            Herbicidally active polypeptide SEQ ID NO 2459.
                                                                                                                                                                                                                                                                                                                                                          Herbicidal; plant; agriculture; herbicide
                                                                                                                                                                                                                                            ABB93248 standard; Protein; 382 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-AUG-2001; 2001WO-EP09892
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126; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -QMLNLAFRDCNWVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSN 236
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990S-0151066
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99US-0145224
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20 MAY 1999;
21 MAY 1999;
25 MAY 1999;
25 MAY 1999;
27 MAY 1999;
01 JUN 1999;
03 JUN 1999;
04 JUN 1999;
07 JUN 1999;
07 JUN 1999;
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10 JUN 1999;
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19-JUL-1999;
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20-JUL-1999;
20-JUL-1999;
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15-JUL-1999;
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                                                                                                                                                                                                                                                                                                         297 NENK----DER--QVTBLKLLMD-VHMACIINGKERKBEDWKKLFMBAGFQSYKISPFT 348
                      122 YFLEPNCQGAWNQLKRW----VHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDS 177
                                                      236
                                                                                                                                                                   253
                                                                                                                                                                                                             237 NLTFVGGDMFKCIPKADAVLLKLVLHNWNDNDCMKILBNCKEAISGESKTGKVVVIDTVI 296
                                                                                                                                                                                                                                           254 GVENVEGDMFDSIPACDAIFIKWVLHDWGDKDCIKILKNCKEAV--PPNIGKVLIVESVI 311
                                                                                                                                                                                                                                                                                                                                       312 GENKKTMIVDERDEKLEHVRLMLDMVMMAHTSTGKERTLKEMDFVLKEAGFARYEVRDID 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                               178 -OMINLAFRDCNWVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSN
                                                                                                                                                  Arabidopsis thaliana protein fragment SEQ ID NO: 33864.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG28589 standard; Protein; 368 AA.
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990S-0123180.
990S-0123180.
990S-0125788.
990S-01267824.
990S-0127462.
990S-0127462.
990S-0127462.
990S-0129845.
990S-0130891.
990S-0130891.
990S-0131049.
990S-0131048.
990S-0132484.
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99US-0134218.
99US-0134219.
99US-0134221.
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99US-0134768.
99US-0134941.
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                                                                                                                                                                                                                                                                                                                                                                                                          349 GYLSLIEIY 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                      372 DVQŠLÍIAY 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    termination sequence
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16-APR-1999;
19-APR-1999;
21-APR-1999;
23-APR-1999;
23-APR-1999;
28-APR-1999;
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01-APR-1999;
06-APR-1999;
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05-MAR-1999
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30-APR-1999
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07-MAY-1999
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SASPSHLRRI---MRFLVHQGIFKEIPTKDGLATGYVNTPLSRRLMITRRDGKSLAPFVL 119
                                                                                                                                                                                                                                                                                                                          -OMINIAFRDCNWVFBGLBSIVDVGGGTGITAKIICBAFPKLKCMVLBRPNVVBNLSGSN 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    297 NENK-----DER--QVTELKLLMD-VHWACIINGKERKEEDWKKLFMEAGFQSYKISPFT 348
                                                                                                                                                                                                                                       65 QVPPTKTRQVQSLMRYLAHNGFFEIVRIHDNI-BAYALTAASE--LLVKSSELSLAPMVE 121
                                                                                                                                                                                                                                                                                                      122 YFLEPNCQGAWNQLKRW----VHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 GVENVEGDMFDSIPACDAIFIKWVLHDWGDKDCIKILKRNCKEAV--PFNIGKVLIVESVI 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 GENKKTMIVDERDEKLEHVRLMLDMVYMAHTSTCKERTLKEWDFVLKEAGFARYEVRDID 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                              6 NNGRKA-SEIFQGQALLYKHLLGFIDSKCLKWMVELDIPDIIHSHSGQPITFSELVSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                      237 NLTFVGGDMFKCIPKADAVLLKLVLHNWNDNDCMKILBNCKEAISGESKTGKVVVIDTVI
                                                                                                                                            Gaps
                                                                                                                                          22;
                                                                                                           Length 368;
                                                                                                      27.6%; Score 521; DB 21; Length 36 llarity 33.9%; Pred. No. 1.1e-45; Conservative 70; Mismatches 152; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG28588 standard; Protein; 382 AA.
      990S-0161361.
990S-0161920.
990S-0161992.
990S-0161993.
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990S-0123180.
990S-0123548.
990S-0125788.
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99US-0127462.
99US-0128234.
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99US-0130077.
99US-0130449.
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125; Conserv
      26-0CT-1999;
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29-0CT-1999;
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09-MAR-1999;
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01-APR-1999;
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25-MAR-1999;
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08-APR-1999;
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Matches
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9905-0147302-0905-0147302-0905-0147302-0905-0147302-0905-0147302-0905-0147303-0905-0147303-0905-0147303-0905-0147303-0905-0148341-0905-0148341-0905-0148341-0905-0148341-0905-0148341-0905-0148341-0905-0148341-0905-0148341-0905-0148341-0905-0148341-0905-0148341-0905-0148341-0905-0148341-0905-0148341-0905-0148341-0905-0148341-0905-0148341-0905-0148341-0905-0148341-0905-0148341-0905-0148341-0905-0148341-0905-0148341-0905-0155436-0905-0155438-0905-0155438-0905-0155433-0905-0155438-0905-0155438-0905-0155438-0905-0155438-0905-0155438-0905-0155438-0905-0155438-0905-0155438-0905-0155438-0905-0155438-0905-0155438-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-0905-015928-090
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PR 22-ARR-1599 9990 01100110.

PR 26-ARR-1599 9990 01100110.

PR 10-ARR-1599 9990 01100110.

PR 10-ARR-1599 9990 9910 011248.

PR 10-ARR-1599 9910 011248.

PR 11-ARR-1599 9910 01124.

PR 11-A
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27-AUG-1999; 30-AUG-1999; 31-AUG-1999;

14-OCT-1999

20 - 70L - 1999, 20 - 70L - 1999, 21 - 70L - 1999, 22 - 70L - 1999, 22 - 70L - 1999, 22 - 70L - 1999, 23 - 70L - 1999, 23 - 70L - 1999, 24 - 70L - 1999, 25 - 70L - 1999, 26 - 70L - 1999, 27 - 70L - 1999, 27 - 70L - 1999, 28 - 70L - 1999, 29 - 70L - 1999, 20 - 7

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 YFLEPNCQGAWNQLKRW----VHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 FETTPEMLAPWLRLSSVVSSPVNGSTPPPFDAVHGKDVWSFAQDNPFLSDMINEAXACDA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 -QMLNLAFRDCNWVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSN 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237 NLTFVGGDMFKCIPKADAVLLKLVLHNWNDNDCMKILENCKEAISGESKTCKVVVIDTVI 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297 NENK-----DER--QVTELKLLMD-VHMACIINGKERKEEDWKKLFMEAGFQSYKISPFT 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  312 GENKKTWIVDERDEKLEHVRLMLDMVMMAHTSTGKERTLKEWDFVLKEAGFARYEVRDID 371
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27.6%; Score 521; DB 21; Length 382;
Best Local Similarity 33.9%; Pred. No. 1.2e-45;
Matches 125; Conservative 70; Mismatches 152; Indels 2:
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99US-0160981
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; ORGANISM: 26
US-08-845-742-2
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Sequence 4, Appli
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Sequence 12, Appl
Sequence 14, Appli
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Sequence 10, Appli
Sequence 17, Appli
Sequence 274, Appli
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Sequence 16, Appli
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                                                                           November 10, 2003, 03:17:25 ; Search time 26 Seconds (without alignments) 582.588 Million cell updates/sec
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GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
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US-08-204-288-5

US-08-104-288-5

US-09-500-569-16

US-09-500-569-4

US-09-500-569-14

US-09-500-569-14

US-09-500-569-12

US-08-204-288-7

US-09-500-569-12

US-09-500-569-14

US-09-500-569-14

US-09-500-569-10

US-09-500-569-10

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US-09-615-192A-275

US-09-615-192A-270

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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match Length
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US-09-382-027-3	US-09-059-522-1	US-09-382-027-1	US-09-266-965-3	US-09-252-991A-20452	US-09-252-991A-20476	US-09-500-569-20	US-09-266-965-5	US-08-266-451B-20	US-08-748-725-20	US-09-266-965-4	US-09-004-838-88	US-08-540-804-16	US-08-218-265-16	US-08-521-872-16	US-08-590-399-16	US-08-449-645A-21	US-08-702-367A-21
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ALIGNMENTS

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US-08-845-742-2

| Sequence 2, Application US/08845742C
| Patent No. 2973229
| GENERAL INFORMATION:
| APPLICANT: Walton, Jonathan D
| APPLICANT: Walton, Jonathan D
| TITLE OF INVENTION: Gene Encoding Herbicide Safener Binding Protein
| FILE REFERENCE: 6550-00007
| CURRENT PAPLICATION NUMBER: US/08/845,742C
| UNMER OF SEQ ID NOS: 9
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO 2
| LENGTH: 363
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ORGANISM: Zea mays
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APPLICANT: KNIGHT, www., Marc
APPLICANT: VAN MONTAGU, Marc
APPLICANT: 'LEGRAND, Michel
TITLE OF INVENTION: MODIFICATION OF LIGNIN SYNTHESIS IN
                                                                                                                                                         318 CIINGKERKEEDWKKLFMEAGFQSYKISPFTGYLSLIEI 356
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MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
IR/O8/204,288
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9119279.9
FILING DATE: 10-SEP-1991
PRIOR APPLICATION NUMBER: PCT/GB92/01460
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/204,288
FILING DATE: 10-MAR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VAN DOORSSELAERE, Jan
FRITIG, Bernard J.M.
INZE, Dirk G.
JOUANIN, Lise
KNIGHT, Mary E.
VAN MONTAGU, Marc
                                                                                                                                                                                                                                                                                                                             RESULT 3
US-08-204-288-2
Sequence 2, Application US/08204288
; Patent No. 5959178
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TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 LTV-----FEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNWVFEGLESIV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             199 DVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVLLK 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 LKWMVELDIPDIIHSHSHGQPITFSELVSIL----QVPPTKTRQVQSLMRYLAHNGFFE 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 LKSAVELDLLELMAKAGPGAAISPSELAAQLSTQNPEAPVMLDRMLRLLASYSVLNCTLR 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37;
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                                                                                                                                                                                                                                                                                                                         APPLICANT: VAN MONTAGU, Marc
APPLICANT: LEGRAND, Michel
TITLE OF INVENTION: MODIFICATION OF LIGNIN SYNTHESIS IN
TITLE OF INVENTION: PLANTS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION

TLING DATE: 10-MAR-1994

CLASSIFCATION BOTA:

APPLICATION NUMBER: 6B 9119279.9

FILING DATE: 10-SEP-1991

FRIOR APPLICATION NUMBER: BCT/GB32/01460

APPLICATION NUMBER: PCT/GB32/01460

APPLICATION NUMBER: PCT/GB32/01460

ATTORNEY/AGENT INFORMATION:

NAMMS: KOKULIS, Paul N.

REGISTATION NUMBER: 16,773

REFERENCE/DOCKET NUMBER: 206860/SEE36543/UST

TELECOMMUNICATION INFORMATION:

TELEFAX: (202) 861.3000

TELEFAX: (202) 822-0944

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 364 amino acids

"WIDE: AMINO acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCHWARE: Patentin Release #1.0, Version #1.25 SCHRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,288
FILING DATE: 10-MAR-1994
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEE: CUSHMAN DARBY & CUSHMAN, L.L.P.: 1100 New York Avenue, N.W.
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMBUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                            VAN DOORSSELAERE, Jan
FRITIG, Bernard J.M.
RESULT 2
US-08-204-288-5
; Sequence 5, Application US/08204288
; Patent No. 5959178
; GENERAL INFORMATION:
                                                                                                                                                                                                                           INZE, Dirk G.
JOUANIN, Lise
KNIGHT, Mary B.
VAN MONTAGU, Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 30.4
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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APPLICANT:
APPLICANT:
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APPLICANT:
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206 DVGGGTGATVMIVSKYPSIKGINFDLPHVIGDAPTYPGVEHVGGDMFASVPRADAIFMK 265
                                                                                                                                               266 WICHDWSDEHCLKFLKNCYEALPA---NGKVIIAECILPEAPDTSLATKNTVHYDIVMLA 322
                                                                                                        259 LVLHNWNDNDCWKILENCKEAISGESKIGKVVVIDTVINENKDEROVTELKLLMDVHM-A 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 LKWMVELDIPDIIHSHSHGQPITFSELVSILQVPPTKTR----QVQSLMRYLAHNGFFEI 89
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Best Local Similarity 30.4%; Pred. No. 1.3e-30;
Matches 98; Conservative 69; Mismatches 136; Indels 19; Gaps
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205

92

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-----EIVRIHDNIEAYALTAASELLVKSSE-LSLAPMVEYFLEPNCQGAWNQLKRW 138
                                                                                                                        SLKDLPDGKVERL-----YGLAPVCKFLTKNEDGVSVSPLCLMNQDKVLMESWYYLKDA 146
                                                                                                                                                                                                                                                                                                                                       266 WICHDWSDAHCLKFLKNCYDAL---PENGKVILVECILPVAPDTSLATKGVVHVDVIMLA 322
                                                                                                                                                                                                                                                                                                                 LVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDEROVTELKLLMDVHM-A 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 HNGFFEIVRIH------DNIEAYA-----LTAASELLVKSSELSLAPMVEYFLEPNC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 QGAWNQLKRWVHEBDLTVFBVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCN 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 HGFDGISVLVDVGGGTGVTLKMIISRYKHITGVNFDLPHVISQAPSLPGVNHVAGNMFES 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249 IPKADAVLLKLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDERQVTEL 308
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                                                                                                                                                             139 VHEEDLIVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNWVFEGLESIV
                                                                                                                                                                                                                                        DVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 S---FNVVRCSTEAGPGGDPLRRYSPAPVCRWFTAGD-----NHQGSLAPRLMLDVDEDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 LSTWHQWAAAVVSGGPSAFERAHGMPLFEYMGTNHRFNWLFNQAMSQOSMMVMNKLLDRF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 WVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
APPLICANT: Shen, Jennie
TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase Homologs
FILE REFERENCE: Ball 27 US NA
CURRENT APPLICATION NUMBER: US/09/500,569
CURRENT FILING DATE: 2000-02-09
EARLIER APPLICATION NUMBER: 60/119,587
BARLIER FILING DATE: 1999-February-10
NUMBER OF SEQ ID NOS: 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
19.5%; Score 367; DB 4; Length 37
Best Local Similarity 29.7%; Pred. No. 1.3e-29;
Matches 104; Conservative 70; Mismatches 142; Indels
                                                                                                                                                                                                                                                                                                                                                                                          CIINGKERKEEDWKKLFMEAGFOSYKI 344
                                                                                                                                                                                                                                                                                                                                                                                                                    323 HNPGGKERTEKEFEGLAKGAGFQGFEV 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16, Application US/09500569
Patent No. 6329204
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-500-569-16
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                                                                                                                                                    TGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVLLKLVLHN 263
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VRIHDNIEA----YALTAASELLVKSSE-LSLAPMVEYFLEPNCOGAWNOLKRWVHEED 143
                                                                                  203
                                                                                                                                                                                                                             264 WNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDERQVTELKLIMDVFM-ACIING 322
                                   92 CSLKDHPDGKVERLYGLAPVCKFLTKNEDGVSVSPLCLMNQDKVLMESWYYLKDAILDGG 151
                                                                                                                                                                             LTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNWVFEGLESIVDVGGG
                                                                                                            152 IP-FNKAYGMTAFEYHGTDPRFNKVFNKGMSDHSTITMKKILBTYKGFEGLISLVDVGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetic Engineering of Wood Color
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 53202
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
Componers: MS DOS 6.22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.7%; Score 371.5; DB 2; 29.7%; Pred. No. 4.2e-30; ive 69; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: WordPerfect for Windows 5.2 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/715,325
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US60/007727
FILING DATE: 30 NOV 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Michael, Best & Friedrich
STREET: 100 E. Wisconsin Avenue
CITY: Milwaukee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 19,482
REFERENCE/DOCKET NUMBER: 66040/9627
TELECOMMUNICATION:
TELEPHONE: (414) 271-6560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              United States of America
                                                                                                                                                                                                                                                                                                        323 KERKEEDWKKLFMEAGFOSYKI 344
                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08715325
Patent No. 5886243
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Chiang, Vincent L
APPLICANT: Tsai, Chung-Jui
APPLICANT: Podila, Gopi
TITLE OF INVENTION: Genetic E
TITLE OF INVENTION: in Plants
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Gemignani, Joseph A
REGISTRATION NUMBER: 19,4
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Best Local Similarity 29.73
Matches 97; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TYPE: PRT
ORGANISM: Glycine max
FEATURE:
                                                       ; NAME/KEY: UNSURE
; LOCATION: (134)
US-09-500-569-18
                                                                                                                        Query Match
Best Local S
Matches 99
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Patent No. 6329204;
GENERAL INPORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
APPLICANT: Shen, Jennie
TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase Homologs
FILE REFERENCE: BB137 US NA
CURRENT APPLICATION NUMBER: US/09/500,569
CURRENT FILING DATE: 2000-02-09
EARLIER APPLICATION NUMBER: 60/119,587
EARLIER FILING DATE: 1999-February-10
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
LENGTH: 358
                                                                              US-09-500-569-4

Sequence 4, Application US/09500569

Sequence 4, Application US/09500569

Patent No. 6329204

GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase Homologs
TITLE OF INVENTION NUMBER: US/09/500,569

CURRENT PAPLICATION NUMBER: G0/119,587

EARLIER APPLICATION NUMBER: 60/119,587

SALLIER PRING DATE: 1999-February-10

NUMBER OF SEQ ID NOS: 28

SEQ ID NO 4

SEQ ID NO 4
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320 PLRMDVMMLNNLRGGKIRTEQEYAKLAMDSGFSGSFRTTYIFANFWAIEL 369
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Pred. No. 2.2e-29;
7; Mismatches 138; Indels 15
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Best Local Similarity 31.2
Matches 100; Conservative
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; ORGANISM: Glycine max
US-09-500-569-4
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US-09-500-569-18
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Sequence 6, Application US/08991677A

Patent No. 6252135

GENERAL INFORMATION:

APPLICANT: Chiang, Vincent L

APPLICANT: Carraway, Daniel T

APPLICANT: Smeltzer, Richard H

TITLE OF INVENTION Production of Syringyl Lignin in Gymnosperms

FILE REFERENCE: 50617

CURRENT APPLICATION NUMBER: US/08/991,677A

CURRENT FILING DATE: 1997-12-16

EARLIER APPLICATION NUMBER: US 60/033,381

EARLIER PILING DATE: 1996-12-16

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO S: SEQ ID NO S: 11
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                     Length 358;
18.9%; Score 357; DB 4; Length 35 30.7%; Pred. No. 1.38-28; ive 65; Mismatches 140; Indels
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US-08-991-677-6
                                                      Similarity 30.7
99; Conservative
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Matches 100; Conserv
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78 RMLYVLASYSLFTCSİVEDEENNGGOKRVYGLSOVGKFFVRDEDGASMGFLLALLQDKVF 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 LLSSSVLPFV----LHSTIQLEVFEIL-AKSNDTKLSASQIVS--QIPNCKNPDAATMLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 LLYKHLLGFIDSKCLKWMVELDIPDIIHSHSHGQPITFSELVSILQVP
       APPLICANT: KNIGHT, Mary E.
APPLICANT: VAN MONTAGU, Marc
APPLICANT: LEGRAND, Michel
TITLE OF INVENTION: MODIFICATION OF LIGNIN SYNTHESIS IN
TITLE OF INVENTION: PLANTS
NUMBER OF SEQUENCES: 7
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                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
GURRENT APPLICATION NDATA:
APPLICATION NUMBER: US/08/204,288
FILING DATE: 10-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.9%; Score 337; DB 2;
Similarity 27.5%; Pred. No. 1.6e-26;
06; Conservative 76; Mismatches 131.
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                                                                                                                                                                                             1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/204,288 FILING DATE: 10-MAR-1994 CLASSIFICATION: 800 PRIOR APPLICATION DATA: APPLICATION NUMBER: GB 9119279.9 FILING DATE: 10-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGLETRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 206
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 09-SEP-1992
ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 7
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                                                                                                                                                                                                                                            : D. C. RY: U.S.A.
20005-3518
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                                                                                                                                                                                               STREET:
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Best Local S:
Matches 96
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CNWVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMF 246
                                                                                             KCIPKADAVLLKLVLHNWNDNDCMKILENCKEAISGESKIGKVVVIDTVINENKDERQVT 306
                                                                                                                     94 DNIEA-----YALTAASELLVK-SSELSLAPMVEYFLEPNCOGAWNOLKRWVHEEDL 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     264
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                                 196 TYKGFEGLGSVVDVGGGTGAHLNMIIAKYPMIKGINFDLPHVIEEAPSYPGVEHVGGDMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 VELDIPDIIHSHSHGOPITFSELVSILQVPPTKTRQ----VQSLMRYLAHNGFFBIVRIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 IELGIFDIIAKAGEGAKLSAKDIAAKL---PCKNSEGATMLDRILKLLVCHSIIDCTVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 TVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNWVFEGLESIVDVGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 PFNRVH-GKHVFEYSDMNSSFNQLFMAAMTNRATLIMKKIVESYKGFEHLNSLVDVGGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 GITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVLLKLVLHNW
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                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cahoon, Rebecca E. APPLICANT: Rafalski, Antoni APPLICANT: Rafalski, Antoni APPLICANT: Rafalski, Antoni APPLICANT: Shen, Jennie TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase Homologs FILE REFRENCE: BB137 US NA CURRENT APPLICATION NUMBER: US/09/500,569
EARLIER APPLICATION NUMBER: 60/119,587
EARLIER FILING DATE: 1999-February-10
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 354;
                                                                                                                                                                                   ELKLLMDVHM-ACIINGKERKEEDWKKLFMEAGFQSYKISPFTGY 350
                                                                                                                                                                                                                17.9%; Score 338.5; DB 4; Length 26.4%; Pred. No. 1.1e-26; Live 74; Mismatches 147; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    321 NGKERKEEDWKKLFMEAGFQSYKISPFTGYLSLIEIY 357
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                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/09500569 Patent No. 6329204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08204288
Patent No. 5959178
GENERAL INFORMATION:
APPLICANT: VAN DOORSSELAERE, Jan
APPLICANT: RRITIG, Bernard J.M.
APPLICANT: INZE, Dirk G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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89; Conserv
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LENGTH: 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 VHEEDLTV----FEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNWVFBG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LESIVDVGGGTGTTAKLICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKAD 253
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                                                                                    Sequence 14, Application US/09500569
Fatent No. 6329204
GENERAL INFORMATION
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, Antoni
APPLICANT: Shen, Jennie
TILLE REFERENCE: BB1327 US NA
CURRENT FILING DATE: 2000-02-09
EARLIER APPLICATION NUMBER: US/09/500,569
CURRENT FILING DATE: 1999-February-10
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09500569; Patent No. 6329204; Patent No. 722000; Patent No. 722000; Patent No. 722000; Patent No. 722000; Patent No. 72200; Patent No. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 LKWMVELDIPDIIHSHSHGQPITFSELVSILQVP----PTKTRQVQSLMRYLAHNGFFEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.5%; Score 329.5; DB 4; Length 28.0%; Pred. No. 9.4e-26; tive 71; Mismatches 126; Indels
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TYPE: PRT
ORGANISM: Triticum aestivum
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                      191
                                                                                                                                                                                                                                                                                                                                                                                               EGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                           252 ADAVLLKLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKD----ERQVTE 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 C.-STEAGPGGEPPRRRYSPAPVCRLFTAGGNSHRGSLAPSVLFGVDEDYLCTWRQLAAA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139 VHEEDLIVFEVSLGIPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNWVFEGLESIV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --YALTAASELLV---KSSELSLAPMVEYFLEPNCQGAWNQLKRW 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               199 DVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPK-ADAVLL 257
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                                                                                                                   34 LKWMVELDIPDIIHSHSHGOPITFSELVS--ILQVPPTKTRQVQSLMRYLAHNGFFEIVR
                                                                                                                                                                                                                                                                         RWVHEEDLIV-----FEVSLGIPFWDFINKDPAYNKSFNEAMACDSOMLNLAFRDCNWVF
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Stafaski, Antoni
APPLICANT: Shafaski, Antoni
APPLICANT: Shen, Jeanie
TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase Homologs
FILE REFERENCE: BB1327 US NA
CURRENT APPLICATION NUMBER: US/09/500,569
CURRENT APPLICATION NUMBER: 60/119,587
EARLIER APPLICATION NUMBER: 60/119,587
EARLIER PILLING DATE: 1999-February-10
NUMBER OF SEQ ID NOS: 28
                                                  53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26;
    DB 4; Length 356;
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                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           309 VDMIMLAHNP---GGRERYERBFEALAKGAGFKAIK 341
17.1%; Score 322.5; DB 4; 28.0%; Pred. No. 4.9e-25; ive 68; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 308 LKLLMDVHMACIINGKERKEEDWKKLFMEAGFQSYK 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.9%; Score 319; DB 4; 28.9%; Pred. No. 1.2e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/09500569 Patent No. 6329204
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SEQ ID NO 10
LENGTH: 378
                                           94; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Oryza sativa
                   Similarity
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Best Local Similarity
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US-09-500-569-10
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261 DAIFWKWVLHDWSDEHCVKILNKCYESL---AKGGKIILVESLIPVIPEDNLESHMVFSL 317
             DAVLLKLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVI----NENKDERQVTEL 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 HDN----IEAYALTAASELLVKSSELSLAPMVEYFLEPNCQGAWNQLKRWVHEEDLTVFE 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 EDKEGRPORLYGLGPRSKFFLDQNGASTLPTHMLLQEKTLLECWNCLKDAVKEGGADPFT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          209 KIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVLLKLVLHNWNDND 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149 VSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNWVFEGLESIVDVGGGTGITA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 328;
                                                                                                                                                                                                                                                                                   GENERAL INCORMATION:
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Bloksberg, Leonard N.
TILLE GF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content;
FILE REFERENCE: 11000.1003c4U
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT PILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR PILING DATE: 1996-09-11
PRIOR PILING DATE: 1996-09-11
PRIOR PILING DATE: 1996-09-11
STOR PILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 405
SEQ ID NOS: 405
SEQ ID NOS: 405
SEQ ID NOS: 405
SEQ ID NOS: 405
SEQ ID NOS: 405
SEQ ID NOS: 405
SEQ ID NOS: 405
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                                                                                              309 KLLMDVHMACIINGKERKEEDWKKLFMEAGFQSYKI 344
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                                                                                                                                                                                                                                                 Sequence 274, Application US/09615192A Patent No. 6410718
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Best Local S:
Matches 79
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KLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDERQVTELKLLMDVHMA 317
                      93 HDNIEAYALTAASELLVKSSE--LSLAPMVEYFLEPNCQGAWNQL------KRWVH 140
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APPLICANT: Jensen, Richard G.
APPLICANT: Jensen, Richard G.
APPLICANT: Jensen, Richard G.
TITLE OF INVENTION: Transgenic Plants With Enhanced Mannitol
NUMBER OF SEQUENCES: 4
ADDRESSED: Quarles & Brady
STREFT: P.O. Box 2113, First Wisconsin Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
16.1%; Score 303; DB 1; Length 365;
Best Local Similarity 26.5%; Pred. No. 5.4e-23;
Matches 89; Conservative 61; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Microsoft Word, Version #5.5 CURRENT APPLICATION DATA:
                                                                                     318 CIIN---GKERKEEDWKKLFMEAGF 339
                                                                                                            334 MLSNSRGGKERTELEFAKLATDSGF 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 9221490026
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/871,416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/186,833 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                           RESULT 14
US-08-186-833-4
/ Sequence 4, Application US/08186833
Patent No. 5563324
/ GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Seay, Nicholas J. REGISTRATION NUMBER: 27386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (608)251-5000
TELEFAX: (608) 251-9166
INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (608)251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: P.O. BCCITY: Madison STATE: WI
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Similarity
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Best Local S.
Matches 139
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Sequence 103, App
Sequence 102, App
Sequence 182, App
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Appli
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                                                                                                                 November 10, 2003, 03:21:21; Search time 76 Seconds (without alignments) 809.030 Million cell updates/sec
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Sequence 6, 7
Sequence 6, 7
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Sequence 6,
Sequence 7,
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Sequence 1
Sequence 2
Sequence 2
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                                                                                                                                                                                      US-09-868-547-4
1886
1 MASSLNNGRKASEIFQGQAL......FQSYKISPFTGYLSLIEIYP
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| cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/PCUZ_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
             GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-11-361-460-6
US-11-361-460-4
US-09-947-027-6
US-09-947-027-6
US-09-786-78-78-103-6
US-10-289-757-102
US-10-289-757-102
US-10-289-757-102
US-10-289-757-105
US-10-289-757-105
US-10-289-757-105
US-10-289-757-105
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US-10-174-693-274
US-09-953-348-133
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                                                                                                                                                                                                                                                                                                                   644079 segs, 171749292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                 - protein search, using sw model
                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
Match Length
                             Copyright
                                                                                                                                                                                          Pitle:
Perfect score:
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371.5
337.5
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                                                                                   OM protein
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16 273.5 14.5 351 15 US-10-267-255-133 Sequence 133, App 18 225.5 12.0 156 16 US-10-174-693-275 Sequence 275, App 19 225.5 12.0 331 15 US-10-174-693-275 Sequence 275, App 20 225.5 12.0 331 15 US-10-156-761-10380 Sequence 10380, App 22 190.5 11.3 285 12 US-0-769-734-15 Sequence 10380, App 22 196.5 9.9 115 12 US-0-769-734-15 Sequence 270, App 22 166.5 9.9 115 12 US-0-953-348-3 Sequence 31, App 12 US-0-953-348-3 Sequence 31, App 13 15 US-10-137-036-78 Sequence 31, App 13 15 US-10-267-25-3 Sequence 31, App 13 14 US-10-267-25-4 Sequence 32, App 13 15 US-10-267-25-4 Sequence 27, App 14 15 US-10-267-25-4 Sequence 27, App 14 15 US-10-267-25-1 US-10-26
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ALIGNMENTS

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RESULT.

US-10-361-460-5

Sequence 5, Application US/10361460

Sequence 5, Application US/10361460

Publication No. US20030163839A1

Sequence 5, Application Genes Encoding Enzymes for Lignin

MAPPLICANT: Wang, Xun

TITLE OF INVENTION: Genes Encoding Enzymes for Lignin

TITLE OF INVENTION: Biosynthesis and Uses Thereof

PRIOR APPLICATION NUMBER: US/10/361,460

CURRENT PELING DATE: 1997-08-12

NUMBER OF SEQ ID NOS: 85

SEQ ID NO S: 85

SEQ ID NO S: 85

SEQ ID NOS: 85

SED ID
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US-10-361-460-7
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168 SFNBAMACDSQ-MLNLAFRDCNWVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERP 226
               NVVENLSGSNNLTFVGGDMFKCIPKADAVLLKLVLHNWNDNDCMKILENCKBAISGESKT 286
                                                                       GKVVVIDTVINENKDERQVTELKKLAMDVHMACIINGKERKEEDWKKLFMEAGFQSYKISP 346
                                                                                                                                304 GKVIILDVVVGYKQSNIKHQETQVMFDLYMMA-VNGVERDEQEWKKIFTERGFKDYKILP 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 VSILQVPPTKTRQVQSLMRYLAHNGFFEIVRIH-----DNIEA---YALTAASELLVK- 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 --SSELSLAPMVEYFLEPNCQG-----AWNOLKR--------WVHEEDLT 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 VFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQ-MLNLAFRDCNWVFEGLESIVDVGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.1%; Score 567; DB 12; Length 370; 34.7%; Pred. No. 1.8e-49; iive 64; Mismatches 132; Indels 62;
                                                                                                                                                                                                                                                      US-10-361-460-6
Sequence 6, Application US/10361460
Sequence 6, Application US/10361460
Sequence 6, Application US/10361460
GENERAL INFORMATION:
APPLICANT: Helentjaris, Timothy G.
APPLICANT: Wang, Xun
TITLE OF INVENTION: Genes Encoding Enzymes for Lignin
TITLE OF INVENTION: Blosynthesis and Uses Thereof
FILE REFERENCE: 0709
FILE REFERENCE: 0709
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                                                                                                                                                                                       363 VIGDVSVIIEVYP 375
                                                                                                                                                                      347 FTGYLS-LIEIYP 358
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Matches 137; Conservative
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TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-361-460-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 ANLALHPIAISPHAVGICAWFRQEQHDPSPYGLAFRQIPTIWEHADNV------ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 VEYFL-----EPNCQG--AWNQLKR--------WVHEEDLTVFEVSLGTPFW 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 -----NALLNKGLLAESRFLMPIVLRECGDEVFRGIDSLVDVGGGHGGAATIAAA 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   275 NCKEAISGESKTGKVVVIDTVINENKDERQVTELKLIMDVHMACIINGKERKEEDWKKLF 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 DFINKDPAYNKSFNEAMACDSQ-MLNLAFRDC-NWVFEGLESIVDVGGGTGITAKIICEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 FPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVLLKLVLHNWNDNDCMKILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 ASEIFQGQALLYKHLLGFIDSKCLKWMVELDIPDIIHSHSHGQPITFSELVSILQVPPTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 366,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.3%; Pred No. 9.5e-4/,
live 70; Mismatches 125; Indels
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APPLICANT: Bowen, Benjamin A.
APPLICANT: Bowen, Benjamin A.
APPLICANT: Wang, Xun
TITLE OF INVENTION: Benes Encoding Enzymes for Lignin
TITLE OF INVENTION: Biosynthesis and Uses Thereof
FILE REPREBENCE: 0709
CURRENT APPLICATION NUMBER: US/10/361,460
CURRENT FILING DATE: 2003-02-10
FRICA APPLICATION NUMBER: 60/057,082
FRICA REDING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.7%; Score 540.5; DB 1 33.3%; Pred. No. 9.5e-47;
                                                                    APPLICANT: Helentjaris, Timothy G.
APPLICANT: Bowen, Benjamin A.
APPLICANT: Bowen, Benjamin A.
APPLICANT: Wang, Xun
ITLE OF INVENTION: Genes Encoding Enzymes for
ITLE OF INVENTION: Genes Encoding Enzymes for
ITLE OF INVENTION: Biosynthesis and Uses The
FILE REFERENCE: 0709
FILE REFERENCE: 0709
CURRENT RILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: 60/657,082
PRIOR PILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 85
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 7, Application US/10361460
; Publication No. US20030163839A1
; GENERAL INFORMATION:
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; Publication No. US20030163839A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 33.3
Matches 128; Conservative
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ORGANISM: Zea mays
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WESULI 6
US-10-091-009-6
Sequence 6, Application US/10091009
Sequence 6, Application VG/10091009
Sequence 6, Application No. US20020138870A1
GENERAL INFORMATION:
APPLICANT: Chiang, Vincent Lee C.
APPLICANT: Li, Langeng
TITLE OF INVENTION: METHODS FOR SIMULTANEOUS CONTROL OF LIGNIN CONTENT AND
TITLE OF INVENTION: COMPOSITION, AND
TITLE OF INVENTION: COMPOSITION, AND
FILLE OF INVENTION: O66040-9718
CURRENT APPLICATION NUMBER: US/10/091,009
CURRENT FILLING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: 60/230,086
PRIOR FILLING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 6
FEMALE: PARENTING DATE: PARENTING PARENTE: 2000-09-05
SEQ ID NO 6
FORWARD PARENTING PARENTING PARENTING PARENTE: 2000-09-05
SEQ ID NO 6
FORWARD PARENTING PARENTING PARENTING PARENTER PARENTING PARENTER PA
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                                          139 VHEEDLIVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSOMLNLAFRDCNWVFEGLESIV 198
                                                                                                                                                                                                                                                                           259 LVLHNWNDNDCMKILENCKEAISGESKIGKVVVIDTVINENKDERQVTELKLLMDVHM-A 317
                                                                                                                                                                                                                                                                                                               266 WICHDWSDAHCLKFLKNCYDAL---PENGKVILVECTLPVAPDTSLATKGVVHVDVIMLA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88 -----EIVRIHDNIEAYALTAASELLVKSSE-LSLAPMVEYFLEPNCQGAMNQLKRW 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VHEEDLTVFEVSLGTPFWDFINKDPAYNKSFWEAMACDSQMLNLAFRDCNWVFEGLESIV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258
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                                                                           93 SIKDIPDGKVERI-----YGLAPVCKFLTKNEDGVSVSPLCLMNODKVLMESWYYLKDA
                                                                                                                                                          DVGGGTGTTAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVLLK
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                                                                                                                                                                                                                                                                                                                                                                                           318 CIINGKERKEEDWKKLFMEAGFQSYKI 344
                                                                                                                                                                                                                                                                                                                                                                                                                                323 HNPGGKERTEKEFEGLAKGAGFOGFEV 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HNPGGKERTEKEFEGLAKGAGFQGFEV 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CIINGKERKEEDWKKLFMEAGFQSYKI 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: aspen populus tremuloides
US-10-091-009-6
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Matches 9
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IITLE OF INVENTION: CELLULOSE FOR SIMULTANEOUS CONTROL OF LIGNIN CONTENT AND COMPOSITIC
TITLE OF INVENTION: CELLULOSE CONTENT IN PLANTS
FILE REPERENCE: 066040-9718
CURRENT APPLICATION NUMBER: US/09/947,027
CURRENT FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: 60/230,086
PRIOR PILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                           12;
                                                                                                                                                                                                                                                                                                                                                                                                                                               ROVOSLMRYLAHNGFFEIVRIHDNIEAYALTAASELLVKSSELSLAPMVEYF----LEPN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 PFLGRVWRLLVTSGVF---ASSDDVQ-YRLNPLSWLLVEGVESEDHTYQKYFVLGTVSRH 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 CQGAMNQLKRWVHEED-----LTVFEVSLGTPFWDFINK--DPAYNKSFNEAMAC-DSQ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 YVEAGMSLADWFKKEEDEDRQLPSPFBALHGVPLVHESTKLLDBELDRVVEEGVAAHDN1 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 TIT------IPPAQAVMLKLVLHFWSDDDCVKILBLCRKAIPSRQEGGKVIIIEILL 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   297 NENKOBRQVTELKLIMDVHMACIINGKERKEEDWKKLFMEAGFQSYKISPFTGYLSLIEI 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     294 GPYMGP-VMYBAQLLMDWLMMVNTKGRQRGEDDWRHIFTKAGFSDYKVVKKIGARGVIEV 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------EIVRIHDNIEAYALTAASELLVKSSE-LSLAPMVEYFLEPNCQGAMNQLKRW 138
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                                                                                                                                                                                                                                                                                                                                                                179 MLNLAFRDCNW-VFEGLESIVDVGGGTG-ITAKIICEAFPKLKCMVLERPNVVENLSGSN
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                                                                                                                                                                                                                                                                           32;
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                                                                                                                                                                                                              DB 12; Length 354;
                                                                                                                                                                                                        23.1%; Score 435; DB 12; 34.0%; Pred. No. 6e-36; tive 60; Mismatches 147;
SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 4 LENGTH: 354 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: aspen populus tremuloides US-09-947-027-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09947027
Patent No. US20020124281A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Chiang, Vincent Lee C.
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                                                                                                                                                                                                                                                                        Conservative
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Best Local Similarity
Matches 97; Conserv
                                                                                                                                                                                                                                         Similarity
                                                                                                                      ORGANISM: Zea mays
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                                                                                                                                                 US-10-361-460-4
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Best Local S
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SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 103 LENGTH: 360 TYPE: PRT 137 RWVHEEDLTV----FEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNWVF 191

136 SWYYLKDAVLDGGIPPNKAYGMSAFEYHGTDPRFNRVFNEGMKNHSIIITKKLLELYHGF

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6 B 6 B 6

92 IHDNIEAYALTAASELLVKSSELS----LAPMVEYFLEPNCQGA-----WNQ----LK 136

34 LKWMVELDIPDIIHSHSHGQPITFSELVSIL--QVPPTKTRQVQSLMRYLAHNGFFBIVR 91

17.9%; Score 337.5; DB 12; Length 28.6%; Pred. No. 6.3e-26; Live 62; Mismatches 129; Indels

96; Conservative

Similarity

Query Match Best Local S: Matches 96

; ORGANISM: FLolium perenne US-10-289-757-103

33 LKNAIBLGLLBILVA-AGGKSLTPTEVAAKLPSAANPEAPDMVDRILRLLA----

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8 8

Gaps

49;

196 EGLGSLVDVGGGVGATVAAIAAHYPTIKGVNFDLPHVISEAPQFPGVTHVGGDMFKEVPS 255

252 ADAVLLKLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVI----NENKDERQVTE 307

EGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPK 251

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11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88 -----SYSVLICSLRILPDGKIERLYGLAPVCK-FLIRNDDGVSIAALSLMNQDKVL 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 LKWMVELDIPDIIHSHSHGQPITFSELVSILQVPPTKTR----QVQSLMRYLAHNGFFEI
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Sequence 6, Application US/09796256A
Patent No. US20020078477A1
GENERAL INVENMENTON:
APPLICANT: Chiang, Vincent L
APPLICANT: Carraway, Daniel T
APPLICANT: Carraway, Daniel T
APPLICANT: Smeltezer, Richard H
TILLE OF INVENTION: Production of Syringyl Lignin in Gymnosperms
FILE REFERENCE: 50617/c-3532.0
CURRENT APPLICATION WUMBER: US/09/796,256A
CURRENT FILING DATE: 2001-02-28
PRIOR PELING DATE: 1996-12-16
PRIOR FILING DATE: 1996-12-16
PRIOR PAPLICATION NUMBER: 08/991677
PRIOR PAPLICATION NUMBER: 08/991677
PRIOR PELING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.6%; Score 350.5; DB 9; Length 368; 29.0%; Pred. No. 3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      307 ELKLLMDVHM-ACIINGKERKEEDWKKLFMEAGFQSYKISPFTGY 350
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APPLICANT: FORSTEY, Richard L
APPLICANT: Shenk, Michael Andrew
APPLICANT: Shenk, Michael Andrew
APPLICANT: Shenk, Michael Andrew
APPLICANT: Glenn, Matthew
APPLICANT: Glenn, Matthew
APPLICANT: Saulsburry, Kaith Martin
APPLICANT: Hall, Claire
TITLE OF INVENTION: Compositions isolated from forage
TITLE OF INVENTION: Grasses and methods for their use
FILE REFERENCE: 11000.1061U
CURRENT FILING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: 60/337,703
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 130;
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Publication No. US20030180751A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Liquidambar styraciflua
US-09-796-256A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62;
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Best Local S
Matches 100
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RESULT 9

10-289-757-102

1 Sequence 102, Application US/10289757

1 Fublication No. US20030180751A1

1 GENERAL INFORMATION

1 APPLICANT: Giben, John Bryan

1 APPLICANT: Giben, John Bryan

1 APPLICANT: Shenk, Michael Andrew

1 APPLICANT: Shenk, Michael Andrew

2 APPLICANT: Shenk, Michael Andrew

2 APPLICANT: Shenk, Michael Andrew

3 APPLICANT: Shenk, Michael Andrew

3 APPLICANT: Shenk, Michael Andrew

4 APPLICANT: Shenk, Michael Andrew

5 APPLICANT: Shenk, Michael Andrew

5 APPLICANT: Shenk, Michael Andrew

5 APPLICANT: No. US20030105731A17ss, Geoffrey

7 ITLE OF INVENTION: Compositions isolated from forage

7 ITLE OF INVENTION: Grasses and methods for their use

7 ITLE OF INVENTION: Grasses and methods for their use

7 ITLE OF INVENTION: Grasses and methods for their use

7 ITLE OF INVENTION: Grasses and methods for their use

8 FRIOR APPLICATION NUMBER: US/10/289,757

8 CURRENT APPLICATION NUMBER: US/10/289,757

8 CURRENT PLING DATE: 2001-11-07

9 CURRENT PLING DATE: 2001-11-07

9 NUMBER OF EXQ 1D NOS: 218

9 SOFTWARE: PRACE ARRENT PRACED STATES APPLICANT ON SECOND STATES APPLICANT
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63 ILQVP---PTKTRQVQSLMRYLAHNGFFEIVRIHDNIEAYALTAASELLVK----SS 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 RYGAAPVCK-FLTPNEDGVSMAALALMNQDKVLMESWYYLKDAVLDGGIPFNKAYGMSAF 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        217 KLIKCMVLERPNVVENISGSNNLTFVGGDMFKCIPKADAVILKLVLHNWNDNDCMKILENC 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 277 KEAISGESKIGKVVVIDTVINENKDERO----VTELKLLMDVHMACIINGKERKEEDWKK 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GSTAABIAASADEBACLYALQLGSSSILPMTLKNTIBLGLLETLMA-AGGKSLTPTEVAA 60
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                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Content of the state        313 VDMIMLAHNP---GGRERYERFEALARGAGFTGVK 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/337,703
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 218
SOFTWARE: FASEBE OF Windows Version 4.0
                                                                                                                                                                                                                   Sequence 105, Application US/10289757
Publication No. US20030180751A1
GENERAL INFORMATION:
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; Publication No. US20030180751A1
; GENERAL INFORMATION:
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APPLICANT: Forster, Richard L
APPLICANT: Gibson, John Bryan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       336 LARGAGFAGFK 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 361
TYPE: PRT
CRGANISM: Lolium perenne
US-10-289-757-105
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GDAILMKWILHDWSDQHCATLLKNCYDALPAH---GKVVLVECILPVNPEAKPSSQGVFH 312
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252 ADAVLLKLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDERQ----VTB 307
                                                                                                                                                                                                                                                    192 EGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPK 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Forster, Richard L
APPLICANT: Gibson, John Bryan
APPLICANT: Shenk, Michael Andrew
APPLICANT: No. US20030180751A1riss, Geoffrey
APPLICANT: Glenn, Matthew
APPLICANT: Baulsbury, Keith Martin
APPLICANT: Hall, Claire
TITLE OF INVENTION: Compositions isolated from forage
TITLE OF INVENTION: Grasses and methods for their use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKLLMDVHMACIINGKERKEEDWKKLFMEAGFQSYK 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.6%; Score 331.5; DB 12; 28.0%; Pred. No. 2.6e-25; tive 65; Mismatches 128;
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CURRENT FILING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: 60/337,703
PRIOR FOR ID NOS: 218
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 182, Application US/10289757
Publication No. US20030180751A1
GENERAL INFORMATION:
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; ORGANISM: Festuca arundinacea
US-10-289-757-182
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Best Local Similarity 28.0%
Matches 94; Conservative
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                                                                                                                                                                                                                                                                                                                      Length 360;
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                                                                                                                                                                                                                                                                                                                17.4%; Score 328.5; DB 12; Length 27.7%; Pred. No. 5.2e-25; ive 67; Mismatches 127; Indels
           APPLICANT: No. US20030180751Alriss, Geoffrey, APPLICANT: Glenn, Matthew APPLICANT: Saulsbury, Keith Martin APPLICANT: Saulsbury, Keith Martin APPLICANT: Hall, Claim, Compositions isolated from forage TITLE OF INVENTION: Genesses and methods for their use FILE REFERENCE: 11000.1061U
CURRENT APPLICATION NUMBER: US/10/289,757
CURRENT FILING DATE: 2002-11-07
PRIOR PELLING DATE: 2001-11-07
PRIOR PELLING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 218
SOFFWARE PARTSEQ FOR Windows Version 4.0
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APPLICANT: Raman, Suresh Babu
TITLE OF INVENTION: BETA-ALANINE N-METHYLITRANSFERASE
FILE REFERENCE: 5883-205-1CIP
CURRENT APPLICATION NUMBER: US/10/213,473
CURRENT FILING DATE: 2002-08-06
NUMBER OF SEQ ID NoS: 31
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 29, Application US/10213473
Publication No. US20030104598A1
GENERAL INFORMATION:
 Shenk, Michael Andrew
                                                                                                                                                                                                                                                                ORGANISM: Festuca arundinacea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Limonium latifolium
                                                                                                                                                                                                                                                                                                                                                93; Conservative
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Best Local Similarity
Matches 93; Conserv
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LENGIH: 37
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Best Local S
Matches 87
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37 MVELDIPDIIHSHSHGQPITFSELVSİLQVPP--TKTRQVQSLMRYLAHNGFFEIVRIHD 94

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95 NIEA-------YALTAASELLVKSSELSLAPMVEYFLEPNCQ----GAWNQLKRWV 139
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97 HLDTTSSSSSTSERRYCLTEVGQTLVSFDE-SCPSHGAYVLQHQETLLKAMPFLHTAI 155
                                                                                                                                                                                                                                                                                                                                                                                                                   156 LDASTEPFARVNGEPAYQYYGKNDELNKNMQYAMSGVSVPYMKALLGSGYDGFEGVKTLV 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216 DVGGSSGDCLRMIINKYKDIPKAINFDLPEVVAKAPKIPGITHVGGNMFESVPSGDAIFV 275
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140 HEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNW-VFEGLESIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         # AFFLICANI: anavukkala, 11kms | AFFLICANI: anavukkala, 11kms | TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin Content; FILE REFREENCE: 11000-1003c5 | CURRENT APPLICATION NUMBER: US/10/174,693 | CURRENT FILING DATE: 2002-06-18 | PRIOR APPLICATION NUMBER: US 08/975,316 | PRIOR APPLICATION NUMBER: US 08/713,000 | PRIOR FILING DATE: 1996-09-11 | PRIOR APPLICATION NUMBER: US 09/169,789 | PRIOR APPLICATION NUMBER: US 09/169,789 | PRIOR FILING DATE: 1998-10-09 | PRIOR FILING DATE: 2000-07-12 | NUMBER OF SEQ ID NOS: 407 | SEQ ID NOS: 407 | SEQ ID NOS: 407 | ENVANCE: PARCESC for Windows Version 3.0 | ENVANCE: PARCESC for Windows Version 3.0 | ENVANCE: PARCESC for Windows Version 3.0 | ENVANCE: PARCESC for Windows Version 3.0 | ENVANCE: PARCESC for Windows Version 3.0 | ENVANCE: PARCESC for Windows Version 3.0 | ENVANCE: PARCESC for Windows Version 3.0 | ENVANCE: PARCESC for Windows Version 3.0 | ENVANCE: PARCESC for Windows Version 3.0 | ENVANCE: PARCESC for Windows Version 3.0 | ENVANCE: PARCESC for Windows Version 3.0 | ENVANCE: PARCESC for Windows Version 3.0 | ENVANCE: PARCESC for Windows Version 3.0 | ENVANCE: PARCESC for Windows Version 3.0 | ENVANCE: PARCESC for Windows Version 3.0 | ENVANCE: PARCESC for Windows Version 3.0 | ENVANCE: PARCESC for Windows Version 3.0 | ENVANCE: PARCESC for Windows Version 3.0 | ENVANCE: PARCESC for Windows Version 3.0 | ENVANCE: PARCESC for Windows Version 3.0 | ENVANCE: PARCESC for Windows Version 3.0 | ENVANCE: PARCESC for Windows Version 3.0 | ENVANCE: PARCESC for Windows Version 3.0 | ENVANCE: PARCESC for Windows Version 3.0 | ENVANCE: PARCESC for Windows Version 3.0 | ENVANCE: PARCESC for Windows Version 3.0 | ENVANCE: PARCESC for Windows Version 3.0 | ENVANCE: PARCESC for Windows Version 3.0 | ENVANCE: PARCESC for Windows Version 3.0 | ENVANCE: PARCESC for Windows Version 3.0 | ENVANCE: PARCESC for Windows Version 3.0 | ENVANCES
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Publication No. US20030131373a1
GENERAL INFORMATION:
APPLICANT: BLOKSberg, Leonard N.
APPLICANT: Havukkala, Ilkka
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US-10-174-693-274
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Best Local Similarity
Matches 79; Conserv
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85 GFFEIVRIHDNIEAYALTAASELLVKSSELSLAPMVEYFLEPNCQGAWNQLKRWVHEEDL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 TVFEV-----SLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNWV-----FEG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 SFPSTWPTAPRSGSSP-----TRDPKARELFNRAMG-----SVSLTEAGQVAAAYDFSG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 LESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVEN----LSG---SNNLTFVGGDMF 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 KCIPK-ADAVLLKLVLHNWNDNDCMKILENCKEAISGESKIGKVVVIDTVINENKDERQV 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        245 ETIPDGADVYLIKHVLHDWDDDDVVRILRRIATAMKPDS---RLLVIDNLI---DERPA 297
                                                                                                                                                                                                                                                                                                                                                                                           25 LLGFIDSKCLKWMVBLDIPDIIHSHSHGQPITFSELVSILQVPPTKTRQVQSLMRYLAHN
                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 AS-TLFVDLLLLVLVGGAERSESEFAALLEKKGLRVERSLPCGAGPVRIVEI 348
                                                                                                                                                                                                                                                                                                                                                            49;
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 27.0%; Pred. No. 2.2e-19;
Matches 95; Conservative 68; Mismatches 140; Indels 49;
                                                            completed: November 10, 2003, 03:30:38
                                                       US-09-953-348-133
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GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
               Copyright
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using sw model OM protein - protein search, November 10, Run on:

2003, 03:09:40 ; Search time 43 Seconds (without alignments) 800.660 Million cell updates/sec

Title: Perfect score:

US-09-868-547-4 1886 1 MASSLNNGRKASEIFQGQAL......FQSYKISPFTGYLSLIEIYP

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 Total number of hits satisfying chosen parameters: 283308 segs, 96168682 residues Searched:

length: 0 length: 2000000000 s eq Minimum DB Maximum DB

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

caffatte O methylt lignin-bispecific probable caffeate catechol O-methylt hypothetical prote catechol O-methylt probable catechol caffeoyl-CoA O-met hypothetical prote CDS protein F9111. caffeic acid O-met hypothetical prote myo-inositol O-met hypothetical prote hypothetical prote 6a-hydroxymaackiai catechol O-methylt catechol O-methylt catechol O-methylt catechol O-methylt herbicide safener catechol O-methylt catechol O-methylt isoliquiritigenin O-diphenol-O-methylt isoflavone-O-methy
o-methyltransferas isoflavone-7-0-met Description SUMMARIES T09299 T06786 S52015 S52015 T09266 T04963 T04963 T04963 T04967 T01259 T10259 T10259 S40146 JQ2344 E96559 S28612 DB Query Match Length 1237.5 867.5 867.5 652.5 529.5 529.5 327.5 326 322.5 318.5 316.5 303 Score Result No.

hypothetical prote		hypothetical prote		probable 0-methv1t	carminomycin 4-0-m	probable 0-methylt	O-demethylpuromyci	hypothetical profe	polyketide synthas	tomN protein - Str	hypothetical prote	acetviserotonin O-	acetylserotonin O-	acetviserotonin O-	hydroxyneurosporen
G96804	B86344	E86344	C86344	D86344	A47128	F83120	301393	E96653	JC5855	S27696	F70932	A42106	S21265	137463	T50751
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381	373	373	373	373	356	334	376	205	341	494	339	345	346	373	379
15.0	14.8	14.8	14.4	14.4	14.2	13.6	13.4	13.0	12.8	10.7	10.6	10.3	10.2	9.3	0.6
283.5	278.5	278.5	272:5	271.5	268	257	252	245.5	240.5	202	200.5	194	192	176	170.5
7															

ALIGNMENTS

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A, Description: methyltransferase
C, Superfamily: O-methyltransferase
C, Keywords: methyltransferase
                                                                  Query Match
Best Local Similarity 66.5:
Matches 238; Conservative
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Matches 174; Conservative
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     isoflavone-O-methytransferase (EC 2.1.1.-) - alfalfa
C;paccise: Medicago sativa (alfalfa)
C;paccise: Medicago sativa (alfalfa)
C;paccise: Medicago sativa (alfalfa)
C;paccise: T00-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 17-Nov-2000
R;He, X. Z; Reddy, J. T; Dixon, R.A.
R;He, X. Z; Reddy, J. T; Dixon, R.A.
Plant Mol. Biol. 36, 43-54, 1988
A;Title: Stress responses in alfalfa (Medicago sativa L.) XXII. cDNA cloning and cha; R;Cecsion: T09-707
A;Accession: T09-707
A;Accession: T09-707
A;Residues: Preliminary; translated from GB/EMBL/DDBJ
A;Cross-references: EMBL:U97125; NID:g2580539; PIDN:AAC49928.1; PID:g2580540
A;Cross-references: EMBL:U97125; NID:g2580581; PIDN:AAC49926.1; PID:g2580582
A;Cross-references: EMBL:AF000975; NID:g2580581; PIDN:AAC49926.1; PID:g2580582
C;Genetics:
                                                                                                                CDNA cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 o-methyltransferase (EC 2.1.1..) iomt2003 - alfalfa
C;Species: Medicago sativa (alfalfa)
C;Accession: 10-2099 #sequence_revision 11-Jun-1999 #text_change 26-Aug-1999
C;Accession: T02299
R;He, X.Z.; Dixon, R.A.
submitted to the EMBL Data Library, September 1997
A;Reference number: 216642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EYFLEPNCQGAWNQLKRWVHEEDLTVFEVSLGTPFWDFINXDPAYNKSFNEAMACDSQML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MASSLNNGRKASEIFQGQALLYKHLLGFIDSKCLKWMVELDIPDIIHSHSHGQPITFSEL
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A;Molecule type: mRNA
A;Residues: 1-343 <HEX>
A;Cross-references: EMBL;AF023481; NID:g2565272; PID:g2565273
                                                                                                                                                                                                                                                                                                                                                                                                                                                          68.1%; Score 1285; DB 2;
67.6%; Pred. No. 1.7e-95;
1ive 57; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                   A,Note: 7-IOMT(6)
C,Function:
A,Description: methyltransferase
A,Note: elicitor-inducible
C,Superfamily: O-methyltransferase
C,Keywords: methyltransferase
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nes 242; Conservative
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C. Date: 23-Apr.1999 #sequence_revision 23-Apr.1999 #text_change 11-May-2000
C.Date: 23-Apr.1999 #sequence_revision 23-Apr.1999 #text_change 11-May-2000
C.Accession: 106786
R.Wu, Q.; Preisis, C.L.; VanEtten, H.D.
Plant Mol. Biol. 35, 551-560, 1997
A;Title: Isolabation of the cDNAs encoding (+)6a-hydroxymaackiain 3-O-methyltransferase, A;Reference number: Z15813; MUID:98009990; PMID:9349277
A;Accession: T06786
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-360 «WUQ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Description: catalyzes the methylation of (+)6a-hydroxymaackiain to (+)pisatin A; Pathway: the terminal step in the pisatin biosynthesis C; Superfamily: O-methyltransferase
                                                      5
                                                                                                                                                                                                   VSILQVPPTKTRQVQSLMRYLAHNGFFEIVRIHDNIEAYALTAASELLVKSSELSLAPMV 120
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                                                                                                                                                                                                                                                                                                           EYFLEPNCQGAWNQLKRWVHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQML 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:U69554; NID:g1568636; PIDN:AAC49856.1; PID:g1568637 A;Experimental source: cv. Alaska C;Genetics: A.Note: hmm6 C;Function:
                                                                                                                                  58 VSILQVPSSKIGNVRRIMRYLAHNGFFEIITKEE--ESYALTVASELLVRGSDLCLAPMV
                                                                                                                                                                                                                                                                                                                                         NLAFRDCNWVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 VGGDMFTSIPNADAVLLK------DCLRILKKCKEAVTNDGKRGKVTIIDMVIDEKK
                                                                                               1 MASSLNNGRKASEIFQGQALLYKHLLGFIDSKCLKWMVELDIPDIHSHSHGQPITFSEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 NGRKASEIFQGQALLYKHLLGFIDSKCLKWMVBLDIPDIIHSHSHGQPITFSELVSILQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 PPTKTRQVQSLMRYLAHNGFFEIVRIHDN----IEAYALTAASELLVKSSELSLAPMVEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                   15;
Length 343;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6a-hydroxymaackiain methyltransferase (EC 2.1.1.-) - garden pea
                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
DB 2;
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48.7%; Pred. No. 5.8e-62;
ive 60; Mismatches 116;
                           1.1e - 91
                                              55; Mismatches
65.6%; Score 1237.5; 66.5%; Pred. No. 1.1e
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Outstand ferase (EC 2.1.1.-) - maize
C.Species: Zea mays (maize)
C.Species: Zea mays (maize)
C.Species: Zea mays (maize)
C.Species: Zea mays (maize)
C.Species: Zea mays (maize)
C.Species: Zea mays (maize)
C.Species: Zea mays (maize)
C.Species: Zea mays (maize)
C.Species: Zea mays (maize)
R.Held, B.M.; Wang, H.; John, I.; Wurtele, E.S.; Colbert, J.T.
R.Held, B.M.; Wang, H.; John, I.; Wurtele, E.S.; Colbert, J.T.
R.Held, B.M.; Wang, H.; John, I.; Wurtele, E.S.; Colbert, J.T.
A.Reference number: J02.168; MUID:94105316; PMID:8278520
A.Reference number: J02268; MUID:94105316; PMID:8278520
A.Residues: I.364 <HEL>
A.Residues: I.364 <HEL>
A.Residues: Ceferences: GBIL4063; NID:9404069; PIDN:AAA18532.1; PID:9404070
C.Superimental source: root, cv. NKH31
C.Superimental source: root, cv. NKH31
C.Superimental source: methyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 LSKVHLHPSRVSSLRRLMRVLTTTNVFGTQPLGGGSDDDSBPVYTLTPVSRLLIGSQSSQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 LAQIPLAAMVLDPIIVSPFSELGAWFQHELPDPCIFKHIHGRGIWELIKDDAIFDALVND 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57
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C;Species: Pinus radiata (Monterey pine)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-Aug-1999
C;Accession: T09600
R;Wagner, A.; Walden, A.; Narayan, R.; Walter, C.
submitted to the EMBL Data Library, September 1996
A;Reference number: 216762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 AMACDSQML-NLAFRDCNWVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MELSPNNSTDQS-LLDAQLELWHTTFAFMKSMALKSAIHLRIADAI--HLHGGAASLSQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 LSLAPMVEYFLEPNCQGAWNQLKRWVHEE--DLTVFEVSLGTPFWDFINKDPAYNKSFNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VIDTVINENKDERQVTELKLLMDVHWACIINGKERKEEDWKKLFMEAGFQSYKISPFTGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MASSLANGRKASEIFQGQALLYKHLLGFIDSKCLKWMVELDIPDIIHSHSHGQPITFSEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.1%; Score 606; DB 2; Length 36 35.9%; Pred. No. 5.8e-41; ive 74; Mismatches 148; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:U70873; NID:g1568663; PID:g1568664
A;Experimental source: tissue-type male cone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 28.1%; Score 529.5; DB 2; Best Local Similarity 33.5%; Pred. No. 8.6e-35; Matches 131; Conservative 69; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: T09600
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 35.9
Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSLIEIYP 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 catechol O-methyltransferase (EC 2.1.1.6) - barley (Species: Hordeum vulgare (Darley) (Species: Hordeum vulgare (Darley) (Species: Hordeum vulgare (Darley) (Species: Bordeum) (Sp. 194) (Species: 28-Oct-1996 (Hsequence_revision 07-Feb-1997 (Htext_change 05-May-2000 (Spacession: S52015; S41949) (Speciession: Biol. 26, 1797-1806, 1994 (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (Species of Mayer) (S
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A; Residues: 1-390 <GRE>
A; Cross-references: EMBL:X77467
B; Gregersen, P.L.; Christensen, A.B.; Sommer-Knudsen, J.; Collinge, D.B.
submitted to the EMBL. Data Library, February 1994
A; Description: A novel putative O-methyltransferase from barley is induced by fungal )
A; Reference number: S41949
   LAFRDCNWVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFV 241
                                                                                     243
                                                                                                                                                      GGDMFKCIPKADAVLLKLVLHNWNDNDCMKILBNCKEAISGESKIGKVVVIDTVINENKD 301
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                                                                                                                                                                                                                                                                                                  BRQVTELKLIMDVHMACIINGKERKEEDWKKLFWEAGFQSYKISPFTGYLSLIEIYP 358
                                                                                                                                                                                                                                                                                                                                                LAIQENKHVFBGLESLVDVAGGTGGVAKLIHEAFPHIKCTVFDQPQVVGNLTGNENLNFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A)Accession: S41949
A;Molecule type: mRNA
A;Residues: 1.315, "H', 317-390 cGRW>
A;Cross-references: EMBL:X77467; NID:g453243; PIDN:CAA54616.1; PID:g453244
C;Superfamily: O-methyltransferase
C;Keywords: methyltransferase; S-adenosylmethionine
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; Pred. No. 1.2e-44;
67; Mismatches 134; Indels
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39.1%;
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Best Local Similarity 39.1%
Matches 144; Conservative
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RSLIEVOP 390
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11;

Gaps

43;

Indels

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Qy 297 NEMKDEROVTELKILMD-VHMACIINGKERKEEDWKKILFNEAGFGSYKISPFT 348	Query Match 25.7%; Score 485; DB 2; Length 325; Best Local Similarity 32.3%; Pred. No. 2.6e-31; Matches 113; Conservative 64; Mismatches 115; Indels 58; Gaps 8; QY 21 LYKHLIGFIDSKCLKWWUNDIDPIDIHSHSHOOPITFSELUVSILQVPPTKTRQVQSLMRX 80 19 IWRYVFGFADIAAAKCAIDLKIPEAIENHPSSQPVTLSELSSAVSASPSHLRRIWRF 75 QY 81 LAHNGFFEIVRIHDNI-EAYALTAASELLVKSSELSLAPMVEYFLEPNCQGAMRQLKRWV 139 Db 76 LVHQGLFKEVPTKDGLATGYTNTPLSRRMMITK	Oy: 308 LKLLMDVHMACIINGKERKEBDWKKLFMEAGFOSYKISPFTGYLSLIEIY 357
1 MASSLNNGRKAS	RESULT 8 Total 6 Total 6 Total 7 Total	OY 6 NNGRKA-SEIPGCQALLYRHLIGFIDSKCLKMAVELDIPDIHHSHSGOPIPFSELVSIL 64 1. DNKRKVLDEBAKASLDIWKYVPGFADIAARCAIDLKIPFAIENHPSSQPYTLAELSSAV 76 65 QVPPTKTRQVQSLMRYLAHNGFFEIVRIHDNI-EAYALTAASELLVKSSELSLAPMVE 121 Db 77 SASPGHLENMRFLYLAHNGFFEIVRIHDNI-EAYALTAASELLVKSSELSLAPMVE 121 77 SASPGHLENMRFLYLAHNGFFEIVRIHDNI-EAYALTAASELLVKSSELSLAPWVE 121 OY 122 YFLEPNOQGAMNQLKRWVHEEDLTVFFVSLGTPPWDFINKDPRYNKSPNAMACDS 177 Db 134 FETTPEMLAPWLRLSSVVSSPVNGSTPPPFDAVHGKDVWSFAQDNFFLSDMINBAMACDA 193 OY 178 - CMLNLAFRDCNWVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVBLNGSN 236 139 RRVVPRVAGACHGLFDGAVTHWDVGGGTGETMGMLVKEFPWIKGFNFDLPHYIEVABVLD 253 OY 237 NLTFVGGDMFKCIPKADAVLLKLVLHNMNDNDCMKILENCKBAISGESKTGKVVVDTVI 296 254 GVENVEGDMFKCIPKADARLLKLVLHNMNDNDCMKILENCKBAISGESKTGKVVVDTVI 296 254 GVENVEGDMFKCIPKADARLLKLVLHNMNDNDCMKILENCKBAISGESKTGKVVVDTVI 311

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isoliquiritigenin 2'-O-methyltransferase - alfalfa
C;Species: Medicago sativa (alfalfa)
C;Species: Medicago sativa (alfalfa)
C;Date: 16-Uul-1999 #sequence_revision 16-Uul-1999 #text_change 21-Jul-2000
C;Accession: T09617
R;Maxwell, C.A.; Harrison, M.J.; Dixon, R.A.
Plant J. 4, 971-981, 1993
A;Title: Molecular characterization and expression of alfalfa isoliquiritigenin
    259 LVLHNWNDNDCMKILENCKEAISGESKIGKVVVIDTVINENKDERQVTELKLLMDVHM-A 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198
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                                                                                                                                                                                                                                                                                                                  catechol O-methyltransferase (BC 2.1.1.6) - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 09-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 05-May-2000
C;Accession: S36404
R;Legrand, M. submitted to the BMBL Data Library, August 1993
                                                                                                       34 LKWMVBLDIPDIIHSHSHGQPITFSELVSIL----QVPPTKTRQVQSLMRYLAHNGFPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LKSALELDLLELMAKAGPGAAISPSELAAQLSTQNPEAPVILDRMLRLLATYSVLNCTLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 LTV-----FEVSLGTPFWDFINKDPAYNKSFNEAMACDSOMINLAFRDCNWVFEGLESIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: EMBL:L10211; NID:g289126; PIDN:AAB48059.1; PID:g1843462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89 IVRIHDNIBAYALTAASELLVKSSE-LSLAPMVEYFLEPNCQGAWNQ----LKRWVHBED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: 836403
A;Accession: 836404
A;Accession: 836404
A;Residues: 1-364 <LEG>
A;Cross-references: EMBL:X74453; NID:g396590; PID:g396591
C;Superfamily: O-methyltransferase; S-adenosylmethionine
                                                                                                                                                                                            318 CIINGKERKEEDWKKLFMEAGFQSYKISPFTGYLSLIEI 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       318 CIINGKERKEEDWKKLFMEAGFQSYKISPFTGYLSLIEI 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----FTGFARLVAL 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.Reference number: 216778; MUID:94108491; PMID:8281189
A;Accession: T09617
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-372 < MAX.>
A;Cross-references: EMBL:L10211; NID:9289126; PIDN:AAB48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 386.5; DB 2;
Pred. No. 2.4e-23;
64; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HNPGGKERTEKEFEALAKGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 30.1%;
Matches 102; Conservative 6
                                206
                                                                                                                                                                                                          323
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                                                                                                                                                                                                                                                                                                                                                                                       128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 M-ACDSOMINIAFRDCNWVFEGLESIVDVGGGTGIT--AKIICEAFPKIKCMVIERPNVV 229
A; Cross-references: EMBL: AF033496; NID: 92921303; PIDN: AAC12715.1; PID: 92921304
                                                                                                                                                                                                                                                                                                                                                                                                                           PLEPNCQGAWNQLKRWVHE-----EDL---TVFEVSLGTPFWDFINKDPAYNKSFNEA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176
                                                                                                                                                                                                                                                                                                                                      72 RQVQSLMRYLAHNGFFEIVRIHDNIEAYALTAASELLV------KSSELSLAPMVEY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENLSGSN-NLTFVGGDMFKCIPKADAVLLKLVLHNWNDNDCMKILENCKBAISGESKTGK 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VVVIDTVINENKDERQVTELKLLMDVHMACIINGKERKEEDWKKLFMEAGFQSYKISPFT 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89 IVRIHDNIEAYALTAASELLVKSSE-LSLAPMVEYFLEPNCQGAWNQ----LKRWVHEED 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 LTV----FEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNWVFEGLESIV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 AVLDGGIPFNKAYGMTAFEYHGTDPRFNKVFNRGMSDHSTMSMKKILEDYKGFEGLNSIV 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVLLK 258
                                                                                                                                                                                                                                                                                               68
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8
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catechol O-methyltransferase (BC 2.1.1.6) - common tobacco
Cypecies: Nicotiana tabacum (common tobacco)
Cypecies: Nicotiana tabacum (common tobacco)
Cybate: 09-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 05-May-2000
Rybegrand, M.
Rybegrand, M.
A,Reference number: S36403
A,Recession: S36403
A,Recession: S36403
A,Rocession: S36403
A,Rocession: S36403
A,Rocession: S36403
Cycoserate type: mRNA
A,Relevences: 1-364 <LEG>
A,Cross-references: RNBL,X74452; NID:g396588; PID:g396589
C,Superfamily: O-methyltransferase; S-adenosylmethionine
                                                                                                                                                                                                                                                                                                                                                                59 PFLRRLILLLAASGVFTVDKQSSEBERYRISPVSYLLVDGIPHEDHMNHTALVLTCTSTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 SEIFQGQALLYKHLLGFIDSKCLKWMVELDIPDIIHSHSHGQPITFSELVSILQVPPTKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 LKWMVELDIPDIIHSHSHGOPITFSELVSIL----QVPPTKTRQVQSLMRYLAHNGFFE
                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                        40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 364;
                                                                                                                                                          DB 2; Length 363; 1.6e-26;
                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.7%; Score 390.5; DB 2; 30.4%; Pred. No. 1.2e-23; live 64; Mismatches 135;
                                                                                                                                                                                                     Mismatches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Superfamily: O-methyltransferase Keywords: methyltransferase; S-adenosylmethionine
                                                                                                                                                       22.6%; Score 426;
llarity 31.4%; Pred. No. 1
Conservative 70; Mismatche
                  A, Experimental source: strain B73 C, Genetics: 879 C, Genetics: 879 C, Genetics: 879 C, Map position: 2 C, Superfamily: 0-methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GYLSLIEIYP 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GARVAFEVYP 363
                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 103; Conserv
                                                                                                                                                     Query Match
Best Local Simi
Matches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   230
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143

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265

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caffeate O-methyltransferase (BC 2.1.1.68) - alfalfa
C;Species: Medicago sativa (alfalfa)
C;Species: Medicago sativa (alfalfa)
C;Species: Medicago sativa (alfalfa)
C;Species: Medicago sativa (alfalfa)
C;Species: Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T06673
R;Gowri, G; Bugos, R.C.; Campbell, W.H.; Maxwell, C.A.; Dixon, R.A.
Plant Physiol. 97, 7-14, 1991
A;Tile: Molecular cloning and expression of alfalfa S-adenosyl-L-methionine: caffe
A;Reference number: Z16815
A;Reference number: Z16813
A;Status: preliminary, translated from GB/BMBL/DDBJ
A;Status: preliminary, translated from GB/BMBL/DDBJ
A;Status: preliminary, translated from GB/BMBL/DDBJ
A;Residues: 1-365 cGOMs
A;Residues: 1-365 cGOMs
A;Residues: 1-365 cGOMs
A;Residues: Justiniary Surces: Subspecies sativa, cultivar Apollo
C;Runction: A;Pathway: lignin biosynthesis
C;Superfamily: O-methyltransferase; S-adenosylmethionine
            139 LTDAVLDGGVPFNKAYGMTAFEYHGTDPRFNKVFNRGMSDHSTMTMKKILEDYKGFEGLN 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VRIHDNIBA---YALTAASELLVKSSE-LSLAPMVEYFLEPNCQGAWNQ----LKRWVHE 141
                                                                                                                                       256 LLKLVLHNWNDNDCMKILENCKEALSGESKTGKVVVIDTVINENKDERQVTELKLLMDVH
                                                                                                                                                            259 PMKWICHDWSDEHCLKFLKNCYEALPA---NGKVLVAECILPETPDTSAATKNAVHVDIV
                                                                                 SIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 İKSALELDILETİAKAGPGAQİSPIETAS--ÖLPTİNPDAPVMLDRMİRLLACYTİLTCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BDLTV-----FEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNWVFBGLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     197 IVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 LVDVGGGGTGAVINTIVSKYPTIKGINFDLPHVIEDAPSYPGVEHVGGDMFVSIPKADAVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LKLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDERQVTELKLLMDVHM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 20.1%; Score 379.5; DB 2; Best Local Similarity 31.4%; Pred. No. 8.9e-23; Matches 106; Conservative 63; Mismatches 134;
                                                                                                                                                                                                                      316 M-ACIINGKERKEEDWKKLFWEAGFQSYK 343
                                                                                                                                                                                                                                                316 MLAHNPGGKERTEKEFEALAKGAGFTGFR 344
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712259
O-diphenol-O-methyltransferase (EC 2.1.1.-) - pepper
C.diphenol-O-methyltransferase (EC 2.1.1.-) - pepper
C.Species: Capsicum annuum (pepper)
C.Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 11-Jan-2000
C.Accession: T12259
R.Lee, B.; Choi, D.; Lee, K.W.
J. Plant Biol. 41, 9-14, 1998
A.Title: Isolation and characterization of o-diphenol-O-methyltransferase cDNA Clone in A.Reference number: Z17476
A.Accession: T12259
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Residues: 1-359 cLBB-
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: 1-359 cLBB-
A.Status: Dreliminary; translated from GB/EMBL/DDBJ
A.Stross-references: EMBL:U83789; NID:g1791351; PID:g1791352
A.Stross-references: EMBL:U83789; NID:g1791351; C.Superfamily: O-methyltransferase
C.Superfamily: O-methyltransferase
C.Superfamily: O-methyltransferase
                                               of isoliquiritigenin (2',4,4'-trihydroxychalcd is the most potent of the nod-gene-inducing fl
                                                                                                                                                                                                                                                                                                                                                 SDLPNRLDRMLRLLA--SYSVLTSTTRT1EDGGAERVYGLSMVGKYLVPDESRGYLASFT 136
                                                                                                                                                                                                                                                                                                                                                                                                                      MLNLAFRDCNWVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNL 238
                                                                                                                                                                                                                                                                                                            ----QVQSLMRYLAHNGFFEIVRIHDNIE-----AYALTAASELLV-KSSELSLAPMV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           299 NKDERQVTELKLLMDVHWACIINGKERKEEDWKKLFMEAGFQSYKIS--PFTGYLSLIEI 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BPNTSEESKLVSTLDNIMFITVGGRERTEKQYEKLSKISGFSKFQVACRAFNS-LGVMEF 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89 TLRTLPDGRVERLYSLAPVCKLLTRNADGVSVAPLL------LMNQDKVLMBSWYH 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BEDLTV-----FEVSLGTPFWDFINKDPAYNKSFNEAMACDSOMLNLAFRDCNWVFPGLE 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88
                                                                                                                                                                                                                             EYFLEPNCQGAWNQLKRWVHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAM--ACDSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TFVGGDMFKCI PKADAVLLKLVLHNWNDNDCMKILENCKBAISGESKTGKVVVIDTVINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 FFEIVRIHDNIEAYALTAASELLVKSSE-LSLAPMVEYFLEPNCOGAWNQ----LKRWVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----RQVQSLMRYLAHNG
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                                                                                                                                                        Length 372;
                                                                                                                                             20.4%; Score 384; DB 2; Length 37; larity 28.5%; Pred. No. 4e-23; Conservative 77; Mismatches 137; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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A;Experimental source: subspecies sativa; cultivar Apollo C;Function:
A;Description: methylates the 2'-hydroxyl of isoliquiritig A;Note: 4'-dihydroxy-2'-methoxychalcone is the most pote C;Superfamily: O-methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 LKWMVELDIPDIIHSHSHGQPITFSELVSILQVPPTKT--
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Best Local Similarity 31.33
Matches 103; Conservative
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Matches 103;
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Gaps

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

November 10, 2003, 01:53:20 ; Search time 23 Seconds (without alignments) 731.981 Million cell updates/sec

US-09-868-547-4 1886 1 MASSLNNGRKASEIFÇGQAL......FQSYKISPFTGYLSLIEIYP 358 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 127863 seqs, 47026705 residues Searched:

127863

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	60MT COPJA	ZRP4 MAIZE	4OMT COPJA	COMT_COFCA	OMT1_ARATH	COMT_CAPAN	COMT_CATRO	OMT1_CHRAE	COMT_MEDSA	OMT2_CHRAE	COMT CAPCH	COM1_OCIBA	COM1_POPTM	COM1 POPKI	COMT_PRUDU		COM2_OCIBA	COM2_POPTM	COMT_BUCGU	COMT_ROSCH	COMT_CLABR	COMT ZINEL	COMT_SACOF	COMT_EUCGL	SMT_COPJA	COMT_MAIZE	IMT1 MESCR	CM4T_STRPE	DMPM STRLP	TCMN_STRGA	HIOM BOVIN	HIOM HUMAN	HIOM_CHICK
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ASML_HUMAN	OMTA_ASPPA	CRIF_RHOCA	TCMO_STRGA	DYHC CABEL	UMES_YEAST	N120_YEAST	EPA3_HUMAN	SYL2_SULSO	TRME_STAAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                               137
                                                                                                                                  MRYLVHMKLFTKASIDGELR-YGLAPPAKYLVKGWDKCMVGSILAITDKDFMAPWHYLKD 127
                                                                                                                                                            138 WVHEEDLIVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAF-RDCNWVFEGLES 196
                                                                                                                                                                             197 IVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVL 256
                                                                                                                                                                                                                                 :|||||||| : | ||||||::
188 LVDVGGGTGTAVRNIANAFPHIKCTVYDLPHVIADSPGYSEVHCVAGDMFKFIPKADAIM 247
                                                                                                                                                                                                                                                                257 LKLVLHNWNDNDCMXILENCKEAISGESKTGKVVVIDTVINENKDERQVTELKLLMDVHM 316
                                                                                                                                                                                                                                                                                 77
                                                                                    68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHENYLPROPANOID PRECURSORS.
TISSUE SPECIFICITY: ACCUMILATES PREFERENTIALLY IN THE ROOTS AND IS
LOCATED PREDOMINANTLY IN THE REGION OF THE ENDODERNIS, LOW LEVELS
ARE SEEN IN THE LEAVES, AND OTHER SHOOT ORGANS.
SIMILARITY: TO OTHER OMTS REQUIRING S-ADENOSYL-L-METHIONINE AS
                                                                      11 QAKLWNFIYGFAESLVLKCAVQLDLANII--HNSGTSMTLSELSSRLPSQPVNEDALYRV
                                                                                                         MRYLAHNGFFEIVRIHDNIEAYALTAASELLVKSSELSLAPMVEYFLEPNCQGAWNQLKR
                                                      18 QALLYKHLLGFIDSKCLKMMVELDIPDIIHSHSHGQPITFSELVSILQVPPTKTRQVQSL
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ,,
     Length 347;
             Pred. No. 5.2e-44;
70; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                           358
                                                                                                                                                                                                                                                                                                                                                     346
                                                                                                                                                                                                                                                                                                                                      305 MLNTGGKERTEESWKKLIHDAGYKGHKITQITAVQSVIEAYP
                                                                                                                                                                                                                                                                                                                       317 ACIINGKERKEEDWKKLFMEAGFQSYKISPFTGYLSLIEIYP
  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  v1-rrb-1996 (Rel. 33, Last sequence update) 01-0CT-1996 (Rel. 34, Last annotation update) 0.methyltransferase ZRP4 (EC 2.1.1.-) (OMT).
                                                                                                                                                                                                                                                                                                                                                                                                                    364 AA
33.7%; Score 636.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001601; Methyltransf.
InterPro; IPR001077; O_Metransf2.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                38.98;
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PIR; JQ2268; JQ2268.
                           133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 33, (Rel. 33, I
               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mays (Maize)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MaizeDB; 63528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4577
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 Query Match
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MAIZE
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                           SB LSKVHLHPSRVSSLRRLMRVLTTTNVFGTQPLGGGSDDSEPVYTLTPVSRLLIGSQSSQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSLAPMVEYFLEPNCQGAWNQLKRWVHEE--DLTVFEVSLGTPFWDFINKDPAYNKSFNE 171
                                                                                                                                                                                                                                                                                                                                                                                                         118 LAQTPLAAMVLDPTIVSPFSBLGAWFQHBLPDPCIFKHTHGRGIWELTKDDATFDALVND 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 NLSGSNNLTFVGGDMFKCIPKADAVLLKLVLHNWNDNDCMKILENCKEAISGESKTGKVV 290
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                                                                                                                                                                                             1 MASSLANGRKASEIFQGQALLYKHLLGFIDSKCLKWMVELDIFDIIHSHSHGQPITFSEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 AMACDSOML-NLAFRDCNWVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIDTVINENKDERQVTELKLIMDVHMACIINGKERKEEDWKKLFMEAGFQSYKISPFTGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MELSPNNSTDQS-LLDAQLELWHTTPAFMKSMALKSAIHLRIADAI--HLHGGAASLSQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
3'-hydroxy-N-methyl-. (S)-coclaurine 4'-0-methyltransferase
(EC 2.1.1.116) (S-adenosyl-1-methionine:3'-hydroxy-N-methylcoclaurine 4'-0-methyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3'-hydroxy-N-methyl-S)-coclaurine = 8-adenosyl-L-homocysteine + (8)-reticuline.
PATHWAY: CARRIES OUT & STEP IN THE CONVERSION OF 3'-HYDROXY-N-METHYLCOCLAURINE TO RETICULINE, AN IMPORTANT INTERMEDIATE IN
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coptis japonica (Japanese goldthread).
Wakaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, Ranunculales,
Ranunculaceae, Coptis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20390108; PubMed=10811648; Moriabing T., Tsujita T., Yamada Y., Sato F.; Moriabing T., Tsujita T., Yamada Y., Sato F.; Molecular characterization of the S-adenosyl-L-methionine: 3'-hydroxy-N-methylocalaurine 4'O-methyltransferase involved in isoquinoline alkaloid biosynthesis in Coptis japonica."; J. Biol. Chem. 275:23389-23465(2000).
-- FUNCTION: CATALYZES THE TRANSFER OF THE METHYL GROUP TO THE HYDROXYL GROUP OF 3'-HYDROXYN-N-METHYLCOCLAURINE TO PORM
                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT: Homodimer.
-!- SIMILARITY: BELONGS TO THE METHYLTRANSFERASE SUPERFAMILY.
                                                                                                               Length 364;
                                                                FB8AD93AD5A6611D CRC64;
                                                                                                         32.1%; Score 606; DB 1; L. 35.9%; Pred. No. 1.6e-41; .ive 74; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 350 AA
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                      Pfam; PF00891; Methyltransf 2; 1.
Transferase; Methyltransferase.
                                                                   39583 MW;
InterPro; IPR000051; SAM_bind.
                                                                                                                                               Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSIIEVYP 364
                                                                364 AA;
                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                   114
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                                                                SEQUENCE
                                                                                                           Query Match
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40MT_COPJA
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                                                                                                                                                                                                                                                                                                                                                                                                                       SLMRYLAHNGFFEIVRIHDNIEAYALTAASELLVKSSELSLAPMVEYFLEPNCQGAWNQL 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 RILRYLVKMEILRVEKSDDGQKKYALEPIATLLSRNAKRSMVPMILGMTQKDFMTPWHSM 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192 EGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187 QGIDSLVDVGGGNGTTVKAISDAFPHIKCTLFDLPHVIANSYDLPNIERIGGDMFKSVPS 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADAVLLKLVLHNWNDNDCMKILBNCKEAISGESKIGKVVVIDTVINENKDERQVTELKLL 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 AQAIILKLIHDWNDEDSIKILKQCRNAVPKDG--GKVIIVDVALDEESD-HELSSTRLI 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KRWVHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSOMLNLAF----RDCNWVF 191
the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                               75
                                                                                                                                                                                                                                                                                                                                                                                 13 KAQAHVWKIIYGFADSLVLRCAVELGIVDIJDNNN--QPMALADLASKLPVSDVNCDNLY 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cinnamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hydroxy-trans-
                                                                                                                                                                                                                                                                                                                                           16 QGQALLYKHLLGFIDSKCLKWMVELDIPDIIHSHSHGQPITFSELVSILQVPPTKTRQVQ
                                                                                                                                                                                                                                                                                                      13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Campa C., Legal L., Khounlotham M., Noirot M., de Kochko A.; "Complete cDNA sequence of a caffeic acid O-methyltransferase from Coffea canephora fruit.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coffee canephora (Robusta coffee).

Sukaryota, Virighplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; Asteridae, lamiids, Gentianales, Rubiaceae, Ixoroideae, Coffeeae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QBLLB9;
15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last nontation update)
15-SEP-2003 (Rel. 42, Last sequence update)
Caffeic acid 3-O-methyltzansferase (EC 2.1.1.68) (S-adenosysl-L-methionine:caffeic acid 3-O-methyltransferase) (COMT) (CAOMT).
                                                                                                                                                                                                                                                                Score 587.5; DB 1; Length 350; Pred. No. 4.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 LDIDMLVNTGGKERTKEVWEKIVKSAGFSGGKIRHIAAIQSVIEVFP 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              312 MDVHMACIINGKERKEEDWKKLFMEAGFQSYKISPFTGYLSLIEIYP 358
                                                                                                                                                                                                                                                                                                        83; Mismatches 132; Indels
                                                                                                                                                                                                                            38775 MW; 547835EBCDEF9182 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   350 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                 Interpro; IPR001601, Methyltransf.
Interpro; IPR001077; O_Metransf2.
                                                                                                                                                                                     Pfam; PF00891; Methyltransf 2; 1.
Transferase; Methyltransferase.
SEQUENCE 350 AA; 38775 MW; 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cinnamate.
PATHWAY: Lignin biosynthesis.
                                                                                                                                                                                                                                                                31.2%;
                                                                                                                                   EMBL; D29812; BAB08005.1; -.
                                                                                                                                                                                                                                                                                                        Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=Fruit, and Leaf;
                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=49390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COFCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136
                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coffea,
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                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197 IVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVL 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257 LKLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDERQVTELKLLMDVHM 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 LINILADGGVERLYGLAPVCKFLTKNADGVSMAPIL------LMNQDKVLMESWYHL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 BDLTV-----FBVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNWVFFGLES 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 KDAVLDGGIPFNKAYĞMTAFEYHGTDPRFNKVFNQGMSNHSTITMKKILEVYRGFEGLKT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 VVDVGGGTGATLNMIISKYPTIKGINFELPHVVEDAPSHSGVEHVGGDMFVSVPKGDAIF 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 LKWMVELDIPDIIHSHSHGQPITFSELVSILQVP---PTKTRQVQSLMRYLAHNGFFE-- 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 LKSAIELDLLELIAKAGPGAYVSPSELAA--QLPTHNPEAPIMLDRILRLLATYSVLDCK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89 IVRIHD-NIE-AYALTAASELLVKSSE-LSLAPMVEYFLEPNCQGAMNQ----LKRWVHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiphantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Surantophyta; Massicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=cv. C24; TISSUE=Leaf;
MEDLINE=98007866; PubMed=3349713;
Zhang H., Wang J., Goodman H.M.,
"An Arabidopsis gene encoding a putative 14-3-3-interacting protein,
-!- SIMILARITY: Belongs to the methyltransferase superfamily. Family
                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 350;
                                                                                                                                                                             EMBL; AF454631; AAN03726.1; --
EMBL; AF454632; AAN03725.1; --
InterPro; IPR001601; Methyltransf.
InterPro; IPR001607; O Metransf2.
InterPro; IPR000601; SAM Dind.
Pfam; PF00891; Methyltransf 2; I.
Lignin blosynthesis; Transferase; Methyltransferase.
CONFLICT 230 230 S -> P (IN REF. 1; AAN03726).
CONFLICT 268 268 K -> R (IN REF. 1; AAN03726).
                                                                                                                                                                                                                                                                                                                                                                                                                  .6e-24;
es 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              363 AA
                                                                                                                                                                                                                                                                                                                                                                                                                30.8%; Pred. ....
                                                                                                                                                                                                                                                                                                                                                                                                   20.7%; Score 390.5; 30.8%; Pred. No. 3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    317 -ACIINGKERKEEDWKKLFMEAGFQSYK 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           308 LAHNPGGKERTEKEFEALAKGAGFKEFR 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OMI1 OR ATSG54160 OR K18G13.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                       101, Conservative
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    COMT subfamily.

                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            methyltransferase)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OMT1 ARATH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arch. Blochem. Blophys. 375:385-388(2000).
-!- FUNCTION: Methylates OH residues of flavonoid compounds. Substrate preference is quercetin > myricetin.> luteolin. Dihydroquercetin is not a substrate. Has an optimal pH of 7.5.
-!- CATALYTIC ACTIVITY: Sadenosyl-L-methionine + 3,5,7,3',4'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20166962; PubMed=10700397; Muzac I., Wang J., Anzellotti D., Zhang H., Ibrahim R.K.; "Functional expression of an Arabidopsis cDNA clone encoding a flavonol 3'-0-methyltransferase and characterization of the gene
                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=cv. Columbia,
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.,
"RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by i
SSP consortium (Salk/Stanford/PGEC).",
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: S-adenosýl-L-meřhionine + 3,5,7,3',4'-pentahydroxyflavone = S-adenosyl-L-homocysteine + 3-methoxy-5,7,3',4'-tetrahydroxyflavone.

BNZYME REGULATION: Does not require magnesium. Completely inhibited by 5 mM of either NiSO4 or p-chloromercuribenzoate
                                                                                                                                                                                                                                             "Structural analysis of Arabidopsis thaliana chromosome 5. VI. Sequence features of the regions of 1,367,185 bp covered by 19 physically assigned Pl and TAC clones.";
DNA Res. 5:203-216(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Delseny
caffeic acid/5-hydroxyferulic acid O-methyltransferase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [4]
SEQUENCE OF 285-363 FROM N.A.
SEQUENCE OF Columbia; TISSUE-Green siliques;
STRAIN-cv. Columbia; TISSUE-Green siliques;
Raynal M., Grellet F., Laudie M., Meyer Y., Cooke R., DeSubmitted (OCT-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B4380028D89C43DC CRC64;
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D -> N (IN RE
E -> V (IN RE
T -> S (IN RE
V -> C (IN RE
                                      iochim. Biophys. Acta 1353:199-202(1997)
                                                                                                                           STRAIN=cv. Columbia;
MEDLINE=98403884; PubMed=9734815;
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InterPro; IPR001601; Methyltransf.
InterPro; IPR00107; O'Metransf2.
InterPro; IPR000051; SAM bind.
Pfam; PF00891; Methyltransf2.; 1.
Methyltransferase; Transferase.
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EMBL, AAB013887; BABLIS78.1; -.
EMBL, AXO62837; AAA132915.1; -.
EMBL, AXO61565; AAM10127.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION, AND CHARACTERIZATION
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                                                                                                                                                                                                                                                                                                                                                                     [3]
SEQUENCE FROM N.A.
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363 AA;
                                                                                           SEQUENCE FROM N.A.
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Score 390.5; DB 1; Length 363; Pred. No. 3.8e-24;

20.7%;

Query Match Best Local Similarity

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                                                                                                                                -----LISYSVLTCSNRKLSGDGVERIYGLGPVCKY-LIKNBDGVSIAALCLMNQDKV 133
                                                                                                            -----LAPMVEYFLEPNCQGA------WNQ--- 134
                                                                          81
                                   34 LKWMVELDIPDIIHSHSHGQPITFSELVSILQVPPTKTRQVQSLMRYLAHNGFFEIVRIH 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lee B.-H., Choi D., Lee K.-W.,
"Isolation and characterization of o-diphenol-O-methyltransferase cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA from Capsicum annuum.",
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: Catalyzes the conversion of caffeic acid to ferulic acid
and of 5-hydroxyferulic acid to sinapic acid. The resulting
products may subsequently be converted to the corresponding
alcohols that are incorporated into lignins.
-!- CAPALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,4-dihydroxy-trans-
                                                                        -----RILRL-
                                                                                                                                                                                                      TISSUE SPECIFICITY: Fruit. Not expressed in leaf.
DEVELOPMENTAL STAGE: Expression increases during fruit development but decreases during ripening.
                                                                                                                                                                               -LKRWVHEEDLTV-----FEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCN
                                                                                                                                                                                                                                                  189 WVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKC
                                                                                                                                                                                                                                                                                                                         249 IPKADAVLLKLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDERQVTEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cinnamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hydroxy-trans-
       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Belongs to the methyltransferase superfamily. Family
                                                                                                                                                                                                                                                                                                                                                                                               309 KLLMDVHWACII-----NGKERKEEDWKKLFMEAGPQSYKISPFTGYLSLIEI 356
                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=cv. Chungyang, TISSUE=Root,
Kim K.-W., Lee S.-W.,
"Isolation and characterization of caffeic acid O-methyltrasferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantãe, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, lamiids, Solanales, Solanaceae, Capsicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (S-adenosysl-L-comT) (CAOMT).
     59;
                                                                     36 LKSALELDLLEIM--AKNGSPMSPTELASKL---PTKNPEAPVMLD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (COMT)
   119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-527-2003 (Rel. 42, Created)
15-5EP-2003 (Rel. 42, Last sequence update)
15-5EP-2003 (Rel. 42, Last annotation update)
Caffeic acid 3-O-methyltransferase (EC 2.1.1.68)
methionine:caffeic acid 3-O-methyltransferase) (C
 69; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alcohols that are incorporated into lignins. 3,4-dihydroxy-trans-
CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,4-dihydroxy-trans-
cinnamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hydroxy-trans-
                   in no
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots.
Asteridae, lamiids, Gentianales, Apocynaceae, Rauvolfioideae, Vinceae,
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15-5EP-2003 (Rel. 42, Last sequence update)
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16-5EP-2003 (Rel. 43, Last annotation update)
17-5EP-2003 (Rel. 43, Last annotation update)
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EMBL, AF21216; AAG43822.1;

EMBL, AF21216; AAG43822.1;

InterPro; IPR001601; Methyltransf2.

R InterPro; IPR001001; SAW bind.

R Pfam; PF00891; Methyltransf2; 1.

Pfam; PF00891; Methyltransferase.

W Lignin biosynthesis; Transferase Methyltransferase.

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PATHWAY: Lignin biosynthesis. SIMILARITY: Belongs to the methyltransferase superfamily. Family 2. COMT subfamily.
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Lignin biosynthesis; Transferase; Methyltransferase
SEQUENCE 363 AA; 39785 MW; 700D420F98A52E35 CRC(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 383.5; DB 1;
Pred. No. 1.4e-23;
71; Mismatches 117;
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28-FBB-2003 (Rel. 41, Last sequence update)
15-SBP-2003 (Rel. 42, Last annotation update)
Quercetin 3-O-methyltransferase 1 (EC 2.1.1.76)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AY028439; AAK20170.1; -
InterPro; IPR001601; Methyltransf.
InterPro; IPR001077; O Metransf2.
InterPro; IPR000651; SAM_bind.
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Best Local Similarity 29.3:
Matches 98; Conservative
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                                                                                                                                                                                                                                           CC 5,7,3',4'-
Dentahydroxyflavone = S-adenosyl-L-methionine + 3,5,7,3',4'-
Dentahydroxyflavone = S-adenosyl-L-homocysteine + 3-methoxy-
S,7,3',4'-terrahydroxyflavone.
CC -!- FATHWAY: Phenylpropanoid pathway.
CC -!- MISCELLANEOUS: The Vmax value for flavonoid compounds is two to
threefold higher for OWT1 than for OWT2.
CC -!- GNMILARITY: Belongs to the methyltransferase superfamily. Family
C -!- CAUTION: It is not sure if OWT1 and OWT2 are really encoded by two
different genes or if they represent cloning artifacts.
CC -!- CAUTION: In shyltransf.
DR InterPro; IPRO01601; Methyltransf.
R InterPro; IPRO01601; Methyltransf.
R InterPro; IPRO01601; Methyltransf.
R Pfem: PF00891; Methyltransf.
W Methyltransferase: "The Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of the Transferase of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 VRSVDDQRVYGLAPVCKYLTKNQDGVSIAAL-----C--LMNQDKVLMESWYHLKDA 122
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243 ICHDMSDEHCLKLLKNCYDAL---PNNGKVILAECILPEVPDSSLATKGVVHIDVITVAH 299
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                          -!- FUNCTION: Methylates OH residues of flavonoid and phenylpropano compounds and shows a higher affinity for flavonoid than phenylpropanoid substrates. Substrate preference is quercetin (flavonoid) = luteolin (flavonoid) > 5-hydroxyferulic acid (phenylpropanoid) >> apigenin (flavonoid) = kempferol (flavonoid) >> apigenin (flavonoid) = kempferol (flavonoid).
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15-SEP-2003 (Rel. 42, Last annotation update)
Caffeic acid 3-O-methyltransferase (EC 2.1.1.68) (S-adenosysl-L-
methionine:caffeic acid 3-O-methyltransferase) (COMT) (CAOMT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34;
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STRAIN=cv. Apollo,
Gowri G., Bugos R.C., Campbell W.H., Maxwell C.A., Dixon R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tch 20.1%; Score 380; DB 1; Length 343; al Similarity 30.4%; Pred. No. 2.4e-23; 102; Conservative 68; Mismatches 131; Indels :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F43F2D306E18CB1C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 NPGGKERTEKEFEALAKAAGPQGFQVFCNAFNTYI 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               365 AA
Biochem, Biophys, 351;243-249(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAM-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Methyltransferase, Transferase
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P28002;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 264 MKWICHDWSDEHCLKRELKNCYEAL---PDNGKVIVAECILPVAPDSSLATKGVVHIDVIM 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
90 VRIHDNIEA---YALTAASELLVKSSE-LSLAPMVEYFLEPNCQGAWNQ----LKRWVHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 IVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 LKWMVELDIPDIIHSHSHGQPITFSELVSILQVPPTKTRQVQSLMRYLAHNGFFEI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 İKSALELDILEİİAKAGPGAQİSPIĞIAS--ÖLFITINPDAPVMLDRMLRILACYIİLTCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BDLTV----FEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNWVFEGLES
                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Belongs to the methyltransferase superfamily. Family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3D-structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 365;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           se; Methyltransferase; 3
C14B0D75F979C6B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            317 -ACIINGKERKEEDWKKLFMEAGFQSYKI--SPFTGYL 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 379.5; DB 1;
Pred. No. 2.9e-23;
63; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94 VRTQQDGKVQRLYGLATVAKYLVKNEDGVSISAL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam, PF00891, Methyltransf 2; 1.
Lignin biosynthesis, Transferase,
SEQUENCE 365 AA, 39946 MW: C14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDB; IKYW; 28-AUG-02.
PDB; IKXZ; 28-AUG-02.
ILCEPRO; IPR001601; Wethyltransf.
ILLERPO; IPR001077; O Metransf2.
ILLERPO; IPR000051; SAM bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M63853; AAB46623.1; -.
PIR; T09673; T09673.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tch
al Similarity 31.4%;
106; Conservative 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                     2. COMT subfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003
28-FEB-2003
15-SEP-2003
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       243 ICHDWSDEHCLKLLKNCYDAL---PNNGKVILABCILPEVPDSSLATKGVVHIDVITVAH 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 DNIEA------YALTAASELLVKSSE-LSLAPMVEYFLEPNCQGAWNQ----L 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136 KRWVHEEDLIV----FEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNWV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Curry J., Mendoza M., O'Connell M.;
"Nucleotide sequence of a caffeic acid 3-O-methyltransferase gene from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Catalyzes the conversion of caffeic acid to ferulic acid and of 5-hydroxyferulic acid to sinapic acid. The resulting products may subsequently be converted to the corresponding alcohols that are incorporated into lignins.

CHTALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,4-dihydroxy-transcinnamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hydroxy-trans-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 LKMMVELDIPDIIHSHSHGQPITFSELVSILQVPPTKTRQVQSLMRYLAHNGFFEIVRIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Belongs to the methyltransferase superfamily. Family 2. COMT subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Capsicum chinense (Scotch bonnet) (Bonnet pepper).
Wataryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Pagnoliophyta; eudicotyledons; core eudicots; Asteridae; lamiids; Solamales; Solamaceae; Capsicum.
                                                                                                                                                                                                                                                                                                                 15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Caffeic acid 3-O-methyltransferase (EC 2.1.1.69) (S-adenosysl-L-methionine:caffeic acid 3-O-methyltransferase) (COMT) (CAOMT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 359;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               359 AA; 39636 MW; 4A836904EF6D7119 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001601; Methyltransf.
InterPro; IPR001077; O_Metransf2.
InterPro; IPR001051; SAM bind.
Ligni, PF00891; Methyltransf2; 1.
Lignin losynchesis; Transferae; Methyltransferaee.
SEQUENCE 359 AA; 39636 WW, 4A836904EF6D7119 CRCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67; Mismatches 124;
                                                                                319 IINGKERKEEDWKKLFMEAGFQSYKI--SPFTGYL 351
                                                                                                           300 NPGGKERTEKEFEALAKAAGFQGFQVFCNAFNTYI 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6e-23;
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                                                                                                                                                                                                                                                      359
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                                                                                                                                                                                                                                                                                                15-SEP-2003 (Rel. 42, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF081214; AAC78475.1;
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                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Habanero;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Asteridae, lamiio
NCBI_TaxID=80379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Habanero Chile.";
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                                                                                                                                                                                                                                                 CAPCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                   081646;
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COMT_CAPCH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Ehropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72
                                                                                                                                                                                                                                                           MEDLINE=98181116; PubMed=9514654;
Gauthier A., Gulick P.J., Ibrahim R.K.;
"Characterization of two cDNA clones which encode O-methyltransferases for the methylation of both flavonoid and phenylpropanoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAUTION: It is not sure if OWT1 and OWT2 are really encoded by two different genes or if they represent cloning artifacts.
                                                                                                                                                                                                                                                                                                                                                                       Arch. Blochem. Biophys. 351:243-249(1998).

-!- FUNCTION: Methylates OH residues of flavonoid and phenylpropanoid compounds and shows a higher affinity for flavonoid than phenylpropanoid substrates. Substrate preference is quercetin (flavonoid) = luteolin (flavonoid) = 5-hydroxyferulic acid (phenylpropanoid) > caffeic acid (phenylpropanoid) > apigenin (flavonoid) = kempferol (flavonoid).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 VLDGGIPPNKAYGMSSFEYHGTDPRFNKVFNKGMSDHSTITMKKVFQTYQGFQGLTSLVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 VGGGTGATLTMILSKYPTIRCINFDLPHVIBDAPBYPGIBHVGGDMFVSVPKGDAIPMKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKWMVELDIPDIIHSHSHGOPITFS--ELVSILOVP-PTKTROVOSLMRYLA,HNGFFBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90 VRIHDNIEAYALTAASELLVKSSE-LSLAPMVEYFLEPNCQGAWNQ----LKRWVHEEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVLLKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,5,7,3',4'-
pentahydroxyflavone = S-adenosyl-L-homocysteine + 3-methoxy-
5,7,3',4'-tetrahydroxyflavone.
-!- PATHWAY: Phenylpropanoid pathway.
-!- MISCELLANEOUS: The Vmax value for flavonoid compounds is two to threefold lower for OMT2 than for OMT1.
-!- SIMILARITY: Belongs to the methyltransferase superfamily. Family 2. COMT subfamily.
                                                                    Chrysosplenium americanum (Golden saxifrage).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Saxifragales, Saxifragaceae, Chrysosplenium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34;
    (Flavonol 3-0-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8D363A98330FDE4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 379; DB 1; L, Pred. No. 2.9e-23; 68; Mismatches 131;
  (EC 2.1.1.76)
                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAM-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001601; Methyltransf.
InterPro; IPR001077; O Metransf2.
InterPro; IPR000051; SM-bind.
Pfam; PF00891; Methyltransf2.
Methyltransferase; Transferase.
Quercetin 3-0-methyltransferase 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     343 AA; 37868 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U16793; AAA86982.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity conservative
                        methyltransferase
                                                                                                                                                                   NCBI TaxID=36749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  substrate.
                                                                                                                                                                                                                                          TISSUE=Leaf
                                                                                                                                                                                                                                                                                                                                                          compounds."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Matches
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SOLUTION SOL

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89 IVRIHD-NIE-AYALTAASELLVKSSE-LSLAPMVEYFLEPNCQGAWNQ----LKRWVHE 141
FEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIP 250
                         KADAVLLKLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDERQVTELKL 310
                                                                                                        254 KADAIPMKWICHDWSDDHCIKLLKNCYEALPA---NGKVIIVECILPEAPDTSAATKSKV 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 LKWMVELDIPDIIHSHSHGQPITFSELVSILQVPPTKTR---QVQSLMRYLAHNGFFE-- 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 LKSAIELDLLELIKKSGAGAFVSPVDLAA--QLPTTNPDAHVMLDRILRLLTSYAILECR 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Catalyzes the conversion of caffeic acid to ferulic acid and of 5-hydroxyferulic acid to sinapic acid. The resulting products may subsequently be converted to the corresponding alcohols that are incorporated into lignins.

CATALVIIC ACTILITY: S-adenosyl-L-methionine + 3.4-dihydroxy-transcinnamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hydroxy-transcinnamate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PATHWAY: Lignin biosynthesis. SIMILARITY: Belongs to the methyltransferase superfamily. Family
                                                                                                                                                                                                                                                                                                                                                                                                                          (CAOMT-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Asteridae, lamiids, Lamiales, Lamiaceae, Nepetoideae, Ocimeae,
                                                                                                                                                                                                                                                                                                                                                                                                     2.1.1.68) (S-adenosysl-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Nucleotide sequences of two cDNAs encoding caffeic acid O-methyltransferases from sweet basil (Ocimum basilicum)."; (In) Plant Gene Register PGR99-105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Cv. EXM-1;
Wang J., Dudareva N., Kish C.M., Simon J.E., Lewinsohn E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        (COMT-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000051; SAM bind.
Pfam; PF00891; Methyltransf 2; 1.
Lignin blosynthesis; Transferase; Methyltransferase.
SEQUENCE 361 AA; 39528 MW; D6ABC3D6837AAC9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                        methionine:caffeic acid 3-0-methyltransferase 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 371,5; DB 1
Pred. No. 1.3e-22;
                                                                                                                                                             LMDVHM-ACIINGKERKEEDWKKLFMEAGFQSYK 343
                                                                                                                                                                                                     311 HGDIIMLAHNPGGKERTEKDFEALANWGWFSRFR 344
                                                                                                                                                                                                                                                                                                                                       15-82P-2003 (Rel. 42, Created)
15-83P-2003 (Rel. 42, Last sequence update)
15-85P-2003 (Rel. 42, Last annotation update)
Caffeic acid 3-0-methyltransferase 1 (BC 2.1.
                                                                                                                                                                                                                                                                                                       361 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AF154917, AAD38189.1; -.
InterPro, IPR001601, Methyltransf.
InterPro, IPR001077; O_Metransf2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ocimum basilicum (Sweet basil)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.7%;
29.7%;
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                                                                                                                                                                                                                                                                                                       STANDARD;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=39350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cinnamate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pichersky E.;
                                                                                                                                                                                                                                                                                                   OCIBA
                                                                                  251
191
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                               257 LKLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDERQVTELKLLMDVHM 316
                                                                                                                                                                                                                                                                                                                               262 MKWICHDWSDEHCVKFLKNCYDAL---PONGKVILAECVLPEAPDTGLATKNVVHIDVIM 318
: : | | | | : : | | | : : | | | : | | | | TXTLPDGGVERLYGLAPVCKPLTKONEDGVSMAPLT------LMNQDKVLMESWYHL 141
                                                                               142 EDLTV-----FEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNWVFEGLES 196
                                                                                                                                                                                                                            202 VVDVGGGTGATLNMIVSKYPSIKGINFDLPHVIEDAPSYPGVEHVGGDMFVSVPKGDAIF 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tsai C.-J., Mielke M.R., Podila G.K., Chiang V.L.C.;
Submitted (JUL-1997) to the EMBL/GenBank/DBW databases.

-!- EUNCTION: Catalyzes the conversion of caffeic acid to ferulic acid
and of 5-hydroxyferulic acid to sinapic acid. The resulting
products may subsequently be converted to the corresponding
alcohols that are incorporated into lightins.

-!- CATALYTIC ACTIVITY: 5-adenosyl-L-methionine + 3.4-dinydroxy-trans-
cinnamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hydroxy-trans-
                                                                                                                          42 SDAVVDGGIPFNKAYGMTAFEYHGTDPRFNKVFNQGMSNHSTITMKKILETYTGFDGLKT
                                                                                                                                                                               197 IVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95288373; PubMed=7770514;
Tsai C.-J., Podila G.K., Chiang V.L.C.;
"Nuclectide sequence of a Populus tremuloides gene encoding
bispecific caffeic acid/s-hydroxyferulic acid O-methyltransferase.";
Plant Physiol. 107:1459-1459(1995).

    -!- TISSUB SPECIFICITY: Xylem.
    -!- PTM: The N-terminus is blocked.
    -!- SIMILARITY: Belongs to the methyltransferase superfamily. Family

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "cDNA cloning, sequence analysis and seasonal expression of lignin-bispecific caffeic acid/s-hydroxyferulic acid 0-methyltransferase of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caiteic acid 3-0-methyltransferase 1 (BC 2.1.1.68) (S-adenosysl-L-methionine:caffeic acid 3-0-methyltransferase 1) (COMT-1) (CAOMT-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 165-184; 335-346 AND 349-359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Viridiplantae, Streptophyta, Embryophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eu
eurosids I; Malpighiales, Salicaceae, Populus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMI POPTM STANDARD; PRT; 365 AA. 200753; Q43094; Created? STAR-1993 (Rel. 25, Created? Rel. 25, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Caffeic acid 3-0-methyltransferase 1 (EC 2.1.1.68)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bugos R.C., Chiang V.L.C., Campbell W.H.;
                                                                                                                                                                                                                                                                                                                                                                                 317 -ACIINGKERKEEDWKKLFMEAGFQSY 342
                                                                                                                                                                                                                                                                                                                                                                                                                               319 LAHNPGGKERTEKEFQGLAKAAGFKQF 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lant Mol. Biol. 17:1203-1215(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Populus tremuloides (Quaking aspen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PATHWAY: Lignin biosynthesis.
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Similarity
97; Conserv
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Q43609;
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Best Local (
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    (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                  146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayakawa T., Nanto K., Kawai S., Katayama Y., Morohoshi N.;
"Molecular cloning and tissue-specific expression of two genes that
encode caffeic acid O-methyltransferases from Populus kitakamiensis.";
Plant Sci. 113:157-165[1996].
-!- FUNCTION: Catalyzes the conversion of caffeic acid to ferulic acid
                                                                                                                                                                                                                                                                                                  93 SLKDLPDGKVERL-----YGLAPVCKFLTKNEDGVSVSPLCLMNODKVLMESWYYLKDA
                                                                                                                                                                                                                                                                                                                                                                                                                                              LVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDERQVTELKLLMDVHM-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                              266 WICHDWSDAHCLKFLKNCYDAL---PENGKVILVECILPVAPDTSLATKGVVHVDVIMLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alcohols that are incorporated into lignins.
CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,4-dihydroxy-trans-
                                                                                                                                                                                                                                                  VHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNWVFEGLESIV
                                                                                                                                                                                                                                                                                                                                                       DVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVLLK
                                                                                                                                                                                                                                                                                                                                                                                                           cinnamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hydroxy-trans
                                                                                                                                                                                                                              LKWMVELDIPDIHHSHSHGQPITFSELVSILQVPPTKTR----QVQSLMRYLAHNGFF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I, Malpighiales, Salicaceae, Populus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cinnamate.
PATHWAY: Lignin biosynthesis.
SIMILARITY: Belongs to the methyltransferase superfamily. Family
2. COMT subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last amnotation update)
Caffeir acid 3-0-methyltransferase 1 (EC 2.1.1.68) (S-adenosysl-L-methylonine:caffeic acid 3-0-methyltransferase 1) (COMT-1)
                                                                                                                                                                                                        59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and of 5-hydroxyferulic acid to sinapic acid. The resulting products may subsequently be converted to the corresponding
                                                                                                                                                                             DB 1; Length 365;
                                                                                                                                                                                                        Indels
                                                  EMBL, U33171; AAB61731.1; -.
PIR, S18568; S18568
InterPro; IPR001607; O Metransf.
InterPro; IPR001607; O Metransf2.
InterPro; IPR000051; SAM bind.
Pfam; PF00891; Methyltransf2.
Lighni biosynthesis; Transferase; Methyltransferase.
SEQUENCE 365 AA; 39805 MW; A6CECDEA4E0007CD CRC64;
                                                                                                                                                                                                       69; Mismatches 132;
                                                                                                                                                                                         1.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365 AA
                                                                                                                                                                            19.7%; Score 371.5; 29.7%; Pred. No. 1.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CIINGKERKEEDWKKLFMEAGFQSYKI 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HNPGGKERTEKEFEGLAKGAGFQGFEV 349
entities requires a license agreement ( or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Populus kitakamiensis (Aspen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 42, Created)
(Rel. 42, Last seg
                                           EMBL; X62096; CAA44006.1; -.
                                                                                                                                                                                                    97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI TaxID=3698
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                                                                                                                                                                           Query Match
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COM1_POPKI
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CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,4-dihydroxy-transcinnamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hydroxy-transcinnamate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----EIVRIHDNIEAYALTAASELLVKSSE-LSLAPMVEYFLEPNCQGAWNOLKRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 SLKDLPDGKVERL-----YGLAPVCKFLTKNEDGVSVSPLCLMNQDKVLMESWYYLKDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139 VHBEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNWVFEGLESIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  266 WICHDWSDAHCLKFLKNCYDAL---PENGKVILVECILPVAPDTSLATKGVVHVDVIMLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 LKWMVELDIPDIIHSHSHGQPITFSELVSILQVPPTKTR----QVQSLMRYLAHNGFF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 LKTAIELDILEIMAKAGPGAFLSTSEIASHL---PTKNPDAPVMLDRILRLLASYSILTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVLLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259 LVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDERQVTELKLLMDVHM-A
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (S-adenosysl-L-
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Garcia-Mas J., Messeguer R., Arus P., Puigdomenech P.;
"The caffeic acid O-methyltransferase from Prunus amygdalus.";
(In) Plant Gene Register PGR95-006.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 365;
                                                                                                                                                                                                                                                       InterPro; IPR001601; Methyltransf.
InterPro; IPR001077; O Metransf2.
InterPro; IPR001057; SAM bind.
InterPro; IPR001051; SAM bind.
Pfam; PPF0091; Methyltransf2; 1.
Lignin biosynthesis; Transferase; Methyltransferase.
SRQUENCE 365 AA; 39791 MW; D6005B10FB55B83C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (COMT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.5%; Score 368.5; DB 1; 29.7%; Pred. No. 2.2e-22; iive 68; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Caffeic acid 3-O-methyltransferase (EC 2.1.1.68)
methionine:caffeic acid 3-O-methyltransferase) (C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.5%; Score 367.5; DB 1, Length 365; 30.7%; Pred. No. 2.7e-22; ive 65; Mismatches 133; Indels 37; Gaps 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      263 FWKWICHDWSDEHCLKFLKNCYAAL---PDNGKVILGECILPVAPDSSLATKGVVHIDVI 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 SVVDVGGGTGAVLNMIVSKYPSIKGINFDLPHVIEDAPQYPGVEHVGGDMFVSVPKGDAI 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88 EIVRIHD-NIE-AYALTAASELLVKSSE-LSLAPMVEYFLEPNCQGAWNQ----LKRWVH 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 BEDLTV-----FEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNWVFEGLE 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 LKWMVELDIPDIIHSHSHGQPIIFSELVSILQVPPIKIR----QVQSLMRYLAHNGF--F 87
                  PATHWAY: Lignin biosynthesis.
SIMILARITY: Belongs to the methyltransferase superfamily. Family
2. COMT subfamily.
                                                                                                                                                                                                                                                                                                       InterPro, IPR001601, Methyltransf.
InterPro, IPR001077; O Metransf2.
InterPro, IPR000051; SAM bind.
Pfam; PF00891; Methyltransf2; 1.
Lignin biosynthesis; Transferase; Methyltransferase.
SEQUENCE 365 AA; 39762 MW; C8C4BFEETB018087 CRC64;
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Best Local Similarity 30.78
Matches 104; Conservative
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1 MASSLNNGRKASEIFQGQAL......PQSYKISPFIGYLSLIEIYP 358
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Copyright (c) 1993 - 2003 Compugen Ltd.
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radi	024287	024287	10	α	ä	29.	27
inus radi	09syu3	Q9SYU3	10	ω	œ.		56
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176 NLALRDCDFVFDGLESIVDVGGGTGTTAKIICETFPKLKCIVFDRPQVVENLSGSNNLTY 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 VSILQVPSSKIGNVRRLMRYLAHNGFFBIITKEE--ESYALIVASELLVRGSDLCLAPMV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EYFLEPNCQGAWNQLKRWVHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQML 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NLAFRDCNWVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 VGGDMFTSIPNADAVLIKYILHNWTDKDCLRILKKKKEAVTNDGKRGKVTIIDMVIDKKK 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 DERQVTELKILMDVHMACIINGKERKEEDWKKLFMEAGFQSYKISPFTGYLSLIEIYP 358
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296 DENQVTQIKGLMDVNNAC-LNGKERNBEBWKKLFIBAGFQHYKISPLTGFLSLIEIYP 352
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MASSLNNGRKASEIFQGQALLYKHLLGFIDSKCLKWMVBLDIPDIIHSHSHGQPITFSEL
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                                                                                                                                                                                                                                                                            Medicago sativa (Alfalfa).
Bukaryota, Vizidiphantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots, Rosidae,
Surosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae, Medicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98145455; PubMed-9484461;
He X.Z., Reddy J.T., Dixon R.J.;
"Stress responses in allfa (Medicago sativa L). XXII. cDNA cloning
and characterization of an elicitor-inducible isoflavone 7-0-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.1%; Score 1285; DB 10; Length 352; 67.6%; Pred. No. 6.7e-101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53; Indels
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                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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01-JAN-1998 (TrEMBLrel. 05, Last seq.
01-MAR-2002 (TrEMBLrel. 20, Last anno
                                                                                                                                                                                          Created)
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                                                                                                                                          PRT;
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EMBL, U97125, AAC49928.1, -. InterPro. 1PR001601, Methyltransf.
InterPro. 1PR001077, O Metransf2.
Pfam, PF00891, Methyltransf2.
                                                                                                                                                                                                                                                      Isoflavone-O-methytransferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ECVLDPYLSGSYHELKKWIYEEDLTLFGVTLGSGFWDFLDKNPEYNTSFNDAMASDSKLI 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EYFLEPNCQGAWNQLKRWVHBEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQML 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NLAFRDCNWVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTF 240
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       58 VSILOVPSSKIGNVRRLMRYLAHNGFFEIITKEE--ESYALTVASELLVRGSDLCLAPMV 115
                                                    EYFLEPNCOGAWNOLKKWVHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQML 180
                                                                               181 NLAFRDCNWVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTF 240
                                                                                                                                                                     241 VGGDMFKCIPKADAVLLKLVLHNWNDNDCMKILBNCKBAISGESKTGKVVVIDTVINENK 300
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                                                                                                                                                                                                                                                                                                                            DERQVIELKLIMDVHMACIINGKERKEEDWKKLFMEAGFQSYKISPFIGYLSLIEIYP 358
                                                                                                                                                                                                                                                                                                                                                      296 DENOVTOIKLLMDVNMAC-LNGKERNEEEWKKLFIEAGFOHYKISPLIGFLSLIETYP 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   He X. Z., Reddy J.T., Dixon R.A.; "Stress responses in alfalfa (Medicago sativa L). XXII. cDNA cloning and characterization of an elicitor-inducible isoflavone 7-0-methyltransferase.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  352 AA
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EMBL, APPOOPS; AAC49926.1; -.
INTERPROJ. 10 METHYLTANSE.
INTERPROJ. 1PR001077; O.METRANSÉ2.
PEAM, PPOOB91, METHYLTANSÉ2; 1.
METHYLTANSÉERSE; TRANSÉERSE2; 1.
METHYLTANSÉERSES; TRANSÉERSE.
SEQUENCE 352 AA, 39604 MW, 31B95
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01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
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Best Local Similarity 46.25
                                 Conservative
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Best Local Similarity
Matches 174; Conserv
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"A cDNA of an additional member of the isoflavone-O-methyltransferase (IOMT) of an additional member of the isoflavone-O-methyltransferase (BORS)-170; ";
Palant Physiol. 115:1289-1289(1997).
                                                                                                                                                                                                                                            181 NLAFRDCNWVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTF
                                                                                                                                                                                                                                                                                                                                                                 1 MASSI-NGRKPSEIFKAQALLYKHIYAFIDSMSLKWAVEMNIPNII--QNHGKPISLSNL
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Pisuma sativum (Garden pea).
Bukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
                                                                                                                                                                         Gaps
eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
                                                                                                                                                                        15;
                                                                                                                                                    Length 343;
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                                                                                                                               343 AA; 38433 MW; 296665211415C7BB CRC64;
                                                                                                                                                    DB 10;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                   65.6%; Score 1237.5; DB 10
66.5%; Pred. No. 7e-97;
iive 55; Mismatches 50;
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                                                                                       EMBL, AP023481, AAB88294.1; -- interPro; IPR001077; O Metransf2. Pfam, PP00891; Methyltransf_2; 1. Transferase.
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                                                                                                                                                                     Matches 238; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                FLEPNCQGAWNQLKRWVHEE-DLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLN 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNGEHSNELLHAQAHIWNHIFSFINSMSLKSAIQLGIPDII--NKHGYPWTLSELTSALP 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302 BRQVTELKLIMDVHWACIINGKERKEEDWKKLFMEAGFQSYKISPFTGYLSLIEIYP 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 HPSKVNILYRFLRLITHNGFFAKTTVKSNEGERETÄYVLTPSSKLLVSGKSTCLSSLVKG
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                                                                                                                        7 NGRKASEIFQGQALLYKHLLGFIDSKCLKWMVELDIPDIIHSHSHGQPITFSELVSILQV
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                                                                    Gaps
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X MEDDINE=2107325,

X MEDDINE=2107325,

A Lavid N., Wang J., Shalit M., Guterman I., Bar E., Beuerle T.,

A Menda N., Shafir S., Zamir D., Adam Z., Vainstein A., Weiss D.,

A Pichersky E., Lewinschn E.;

A Pichersky E., Lewinschn E.;

T Dhenolic derivatives in rose petals.";

I phenolic derivatives in rose petals.";

I phenolic derivatives in rose petals.";

R EMBL, AFS02433; AAM23004.1;

R InterPro; IPR001601; Methyltransf.

I InterPro; IPR001677; O Metransf.

I InterPro; IPR001671; AM bind.

R Pfam; PF00891; Methyltransf 2; I.

Transferase; Methyltransf 2; I.

Transferase; Methyltransf 2; I.
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      Length 360
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46.2%; Pred. No. 5e-65;
tive 68; Mismatches 119; Indels
                                                                 Indels
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Last sequence update)
Last annotation update)
   DB 10;
                                                             60; Mismatches 116;
46.0%; Score 867.5; DB 48.7%; Pred. No. 2e-65;
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44.9%; Score 847.5; DE larity 45.6%; Pred. No. 1e-63; Conservative 67; Mismatches 1
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Plant Physiol. 129:1899-1907(2002).
BIMBL; AFSO2434; AAM23005.1;
InterPro; IPR001601; Methyltransf.
InterPro; IPR001077; O'Metransf2.
InterPro; IPR000051; SAM bind.
Pfam; PF00891; Methyltransf2; 1.
Transferase; Methyltransf2; 1.
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MEDLINE=22167322; PubMed=12177504;
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                                                                       01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23, Orcinol O-methyltransferase.
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                                                          (TrEMBLrel. 22,
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                             PRELIMINARY;
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                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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01-OCT-2002 (
01-MAR-2003 (
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Best Local Simi
Matches 162;
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            EPNCQGAWNQLKRWVHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQML-NLA
                                                                                     193 INDCKGVFEGLESLVDVGGGTGTLAKAIADAFPHIECTVLDLPHVVADLOGSKNLKYTGG
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                                                                                                                                                                                     304 QVTELKLIMDVHMACIINGKERKEEDWKKLFMEAGFQSYKISPFTGYLSLIEIYP 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=cv. Old Blush;
Cock J.Mark, Scalliet G., Hugueney P.;
Characterisation of a novel O-methyltransferase involved in the biosynthesis of 3,5-dimethoxytoluene and 1,3,5-trimethoxybenzene, major scent components of rose flowers.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
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46.2%; Pred. No. 5e-65;
live 68; Mismatches 119; Indels
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(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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Transferase; Methyltransferase; SEQUENCE 367 AA: 41278 MM.
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Rosales; Rosaceae, Rosoideae; Rosa.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
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                                                                                                                                                                                                                                                                                                                                                                                                 Lavid N., Wang J., Shalit M., Guterman I., Bar E., Beuerle T., Menda N., Shafit S., Zamir D., Adam Z., Vainstein A., Weiss D., Pichersky E., Lewinschn E., "O-methyltransferases involved in the biosynthesis of volatile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 366;
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Last sequence update)
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                                                                                                                       RASHELLQAQAHIWNHIFSFINSLSLKCAVQLDIPDVI--QKHGQPMTLSELVSALPISP
                                                                                                                                                                                     TKTRQVQSLMRYLAHNGFFEIVRIHD-NIEAYALTAASELLVKSSELSLAPMVEYFLEPN
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                                                             RKASEIFQGQALLYKHLLGFIDSKCLKWMVELDIPDIIHSHSHGQPITFSELVSILQVPP
                                                                                                                                                                                                                                                                                                            CQGAWNQLKRWVHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQML-NLAFRD
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      Gaps
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STRAIN=Cv. Lady Hillington;
Cock J.Mark, Scalliet G., Hugueney P.;
Cock J.Mark, Scalliet G., Hugueney P.;
Cock J.Mark, Scalliet G., Hugueney P.;
Cock J.Mark, Scalliet G., Hugueney D.;
Cock J.Mark, Scalliet G., Hugueney D.;
Cock J.Mark, Scalliet G., Hugueney D.;
Diosynthesis of 3,5-dimethoxytoluene and 1,3,5-trimethoxybenzene,
major scent components of rose flowers.";
Submitted (MAR-2002) to FREL/GenBank/DDBJ databases.
EMBL; AJ439744; CAD29556.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosió
eurosids I, Rosales, Rosaceae, Rosoideae, Rosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELKLIMDVHMACIINGKERKBEDWKKLFMEAGFQSYKISPFTGYLSLIEIYP 358
      4,
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   Mismatches 123; Indels
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348 AA; 38982 MW; 24391E70DDB33C09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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   : 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 158; Conservative
   159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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Rosa hybrid cultivar.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .25 EPNCQGAWNQLKRWVHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQML-NLA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 DPVLTTPWNYLSTWFQNEDPTPFDTAHGMTFWDYGNHQPSIAHLFNDAMASDARLVTSVI 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         192 IDDCKGVFBGLESLVDVGGGTGTVAKAIADAFFHIECTVLDLPHVVADLQGSKNLKYTGG 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DMFKCIPKADAVLLKLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDER 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VPPTKTRQVQSLMRYLAHNGFFEIVRI-HDNIEAYALTAASELLVKSSELSLAPMVEYFL 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNGEHSNELLHAQAHIWNHIFSFINSMSLKSAIQLGIPDIINKHG---PMTLSELTSALP
                                                                                                             STRAIN-cv. Old Blush,
Cock J.Mark, Scalliet G., Hugueney P.;
Cock J.Mark, Scalliet G., Hugueney P.;
Charton of a novel O-methyltransferase involved in the biosynthesis of a novel o-methyltoluene and 1,3,5-trimethoxybenzene, two major scent components of rose flowers.";
Submitted (NAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ439742; CAD29459.1;
Transferase; Methyltransferase.
SEQUENCE 366 AA; 41226 MW; CAF4E17D3230D29E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 NNGRKASEIFQGQALLYKHLLGFIDSKCLKWMVELDIPDIIHSHSHGQPITFSELVSILQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRDCNWVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGG
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I, Rosales, Rosaceae, Amygdaloideae, Prunus.
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Mbeguie-A-Mbeguie D., Gomez R.-M., Fils-Lycaon B.;
"Sequence of an O-Methyltransferase from Apricot Fruit (Accession No. U82011). Gene Expression During Fruit Ripening (PGR97-118).";
Plant Physiol. 114:1569-169(1997).

EMBL; U82011; AAB71213.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESIETQLFFDMLMMALVRGQERNEKEWAKLFTDAGFSDYKITPILGLRSLIEVYP 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                                 44.9%; Score 847.5; DB 10; Length 366; 45.6%; Pred. No. 1e-63;
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Last annotation update)
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Pred. No. 7.7e-63;
eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          354 AA
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InterPro, IPR001077; O Metransf2.
InterPro, IPR000051; SAM_bind.
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01-JAN-1998 (TrEMBLrel. 05,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                       SEQUENCE FROM N.A
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                             NCBI_TaxID=74649;
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SEQUENCE
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61 PIHPKKSNCVYRLMRILVHSGFFCRQKLSELDEEGGYVLTDASRLLLKDDPLSARPFLLG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 GGDMFEAIPPTDAILMKWILHDWSDEECIKILQRSKEAITRKEKKGKVIIVDMVMKQKGD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FLEPNCQGAMNQLKRWVHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLN- 181
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Gang D.R., Lavid N., Zubieta C., Chen F., Beuerle T., Lewinsohn E.,
Noel J.P., Pichersky E.;
"Characterization of Phenylpropene O-Methyltransferases from Sweet
Basil: Facile Change of Substrate Specificity and Convergent Evolution
within a Plant OMT Family.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302 BRQVTBLKLLMDVHMACIINGKBRKBEDWKKLFMBAGFQSYKISPFTGYLSLIBIYP 358
                                                                                        Pruncs dulcis (Almond) (Prunus amygdalus).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots, Rosidae,
eurosids I; Rosales, Rosaceae, Amygdaloideae, Prunus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 LAFRDCNWVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFV
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Asteridae; lamids; Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Ocimum.
NCBI_TaxID=39350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 LNNGRKASEIFQGQALLYKHLLGFIDSKCLKWMVELDIPDIIHSHSHGQPITFSELVSIL
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01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Eugenol O-methyltransferase
Commun basilicum (sweet basil).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                 Suelves M., Puigdomenech P.; "Specific mRNA accumulation of a gene coding for an Omethyltransferase in almond (Prunus amygdalus, Batsch) flower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42.3%; Pred. No. 4.0e-00, cive 70; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4CC6F169513F4EA9 CRC64;
                                    Last annotation update)
         Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 757; DB 10;
Pred. No. 4.8e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     357 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant Sci. 134:79-88(1998).
BMB1, AJ221315; CAA1113.1.; -.
INTE-PRO; IPR001601; Methyltransf.
INTE-PRO; IPR001077; O_Metransf2.
Frām; PF00891; Methyltransf2.; 1.
Methyltransferase; Transferase.
SEQUENCE 356 AA, 40206 MW; 4CC6F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 151; Conservative
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      01-AUG-1998 (TrEMBLrel. 01-MAR-2002 (TrEMBLrel.
                                                                    O-methyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                       STRAIN-cv. Texas;
                                                                                                                                                                                                                               NCBI_TaxID=3755;
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Q93WU2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 VIIDDCKGVFEGLESLVDVGGGTGTVAKAIADAFPHIECTVLDLPHVVGDLQGSKNLKYT 240
                                                                                                                         GGDMFEAVPPADTVLLKWILHDWNDEECIKILKRSRVAITSKDKKGKVIIIDMMMENQKG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VPPTKTROVOSLMRYLAHNGFFEIVRI-HDNIEAYALTAASELLVKSSELSLAPMVEYFL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 EPNCQGAWNQLKRWVHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQML-NLA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 DPVLTNPWNYLSTWFQNDDPTPFDTAHGMTFWDYGNHQPSIAHLFNDAMASDARLVTSVI 182
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                                                                 GGDMFKCIPKADAVLLKLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKD 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 NNGRKASEIFQGQALLYKHLLGFIDSKCLKWMVELDIPDIIHSHSHGQPITFSELVSILQ
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Spermatophyta; Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I; Rosales, Rosaceae, Rosoideae, Rosa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=cv. Lady Hillington;
Cock J.Mark, Scalliet G., Hugueney P.;
"Characterisation of a novel O-methyltransferase involved in the
biosynthesis of 3,5-dimethoxytoluene and 1,3,5-trimethoxybenzene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
                                                                                                                                                                                           302 BRQVTBLKLLMDVHMACIINGKBRKBEDWKKLFMBAGFQSYKISPFTG 349
                                                                                                                                                                                                                           Length 348;
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45.1%; Pred. No. 3.8e-61;
live 67; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 major scent components of rose flowers.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ439743; CAD29555.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        348 348
348 AA; 39034 MW; 0AFD4D325A0DBBID CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                   348 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transferase; Methyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosa hybrid cultivar.
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Matches 156; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=128735;
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                                                                                                                                                                                                                                                                               72 CFQRLMRALVNSNFFIEENNSNNQBVCYWLTPASCLLLKEAPLTVTPLVQVVLDPTFTNP 131
                                                                                                                                                                                                                                                                                                                       WNQLKRW-VHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAF-RDCNW 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PKADAVLLKLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDERQVTELK 309
                                                                                                                                                                                                                                                                                                                                                    WHHMSEWFTHEKHATOFEAANGCTFWEKLANEPSKGRFFDEAMSCDSRLIAHVFTKDYKH 191
                                                                                                                                                                                                 72
                                                                                                                                                                                                                             71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O-methyltransferase.
Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Gentianales; Apocynaceae; Rauvolfioideae; Vinceae;
Catharanthus.
                                                                                                                                                                                                                   13 EIFQGQALLYKHLLGFIDSKCLKWMVELDIPDIIHSHSHGQPITFSELVSILQVPPTKTR
                                                                                                                                                                                                                                                             73 QVQSLMRYLAHNGFFEIVRIHDNIE-AYALTAASELLVKSSELSLAPMVEYFLEPNCQGA
                                                                                                                                                                                                                                                                                                                                                                                     VFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schroeder J.; "A flavonol O-methyltransferase from Catharanthus roseus performing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.5%; Score 726.5; DB 10; Length 347; 41.7%; Pred. No. 1.8e-53; cive 73; Mismatches 117; Indels 17;
                                                                                                                                                                   .,
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                                                                                                                                  38.9%; Score 734; DB 10; Length 357;
larity 41.5%; Pred. No. 4.4e-54;
Conservative 75; Mismatches 121; Indels
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Phytochemistry 62:127-137(2003).
EMBL, A7127569; AAM9748.1;
Transferase.
Transfers 347 AA; 38789 MW; 7FB24ACOBC97AB35 CRC64;
                                                                                                       40236 MW; FC050C48BF6D719C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        347 AA
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           EMBL; AF435008; AAL30424.1; -.
InterPro; IPR001601; Methyltransf.
InterPro; IPR001077; Ometransf2.
InterPro; IPR000051; SAM bind.
Pfam; PF00991; Methyltransf 2; 1.
Methyltransferase; Iransferase.
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70 KTRQVQSLMRYLAHNGFFEIVRIHDNIEAYALTAASELLVKSSELSLAPMVEYFLEPN-- 127

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Db 62 KAPVIHRLMRILVAAGYFS----EBFKNVYSLTSLSRILVKNOPLNLR---EFVLSANEI 114

QY 128 --CQGAWNOLKRWYHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLN-LAF 184

Db 115 AEVBG-WNALSEWFQNDVATAFQTAAGKTYWEYLSQD-KYGKNFDQLMATDSLLISKLLI 172

QY 185 RDCWWYFBGLESIVDVGGGTGITAKIICEAFFKLKGWYLERPWYUNLSGSNNLTFVGGD 244

Db 173 PDYNTLFEGIISLVDVGGGTGITAKIICEAFFKLKGWYLERPWYUNLSGSNNLTFVGGD 232

QY 245 MFKCIPKADAVLLKLVLHNWNDDVKILLBNCKEAISGBSKTGKVVIDTVI-NBNKDER 303

QY 245 MFKCIPKADAVLLKLVLHNWNDDVKILLBNCKEAISGBSKTGKVVIDTVI-NBNKDER 303

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QY 245 MFKCIPKADAVLLKLVLHNWNDDVKILLBNCKEAISGBSKTGKVVIVDTVI-NBNKDER 303

QY 245 MFKCIPKADAVLLKLVHDWKDEDSVKILKNCKKAIPEKKGGKVIVDIVLMDSKKHDN 292

QY 304 QVTELKLLMDVHMACIINGKERKEEDWKKLFWBAGFQSYKIFPMLDFRSPIEVYP 347

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Page 1

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GenCore version 5.1.6
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OM nucleic - nu	nucleic search, using sw model
Run on:	November 9, 2003, 23:30:19 ; Search time 4620 Seconds (without alignments) 10271.681 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-868-547-3 1160 1 gtttgctattatggcttcttataaaagttatctttgtgt 1160
Scoring table:	IDENTITY NUC Gapop 10.0 , Gapext 1.0
Searched:	2888711 segs, 20454813386 residues
Total number of	hits satisfying chosen parameters: 5777422
Minimum DB seg Maximum DB seg	length: 0 length: 2000000000
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He,X.Z., Reddy,J.T. and Dixon,R.A.
Stress responses in alfalfa (Medicago sativa L). XXII. cDNA cloning and characterization of an elicitor-inducible isoflavone
7-O-methyltransferase
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He,X.Z., Reddy,J.T., Guo,J.Z. and Dixon,R.A.
Direct Submission
Submitted (32.APR-1997) Plant Biology Divsion, The
Noble Foundation, 2510 Sam Noble Parkway, Ardmore,
Location/Qualifiers
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KKCIVFDRPRVVCBLLSGTNNLSYYGGDWFQSVPKADAVLLKWILHNWTDNDCRRILEKC
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                                                                                                                                                                         Akashi,T., Aoki,T. and Ayabe,S.

Direct Submission

Bubmitted (14-SEP-2002) Shin-ichi Ayabe, Nihon University,

Department of Applied Biological Sciences; Kameino 1866, Fujisawa,

Kanagawa 252-8510, Japan (B-mail:ayabe@brs.nihon-u.ac.jp,

Tel:81-466-84-3703, Fax:81-466-80-1141)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17
  Sawada, Y., Shimada, N., Sakurai, N., Aoki, T. and Ayabe, S
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                  cDNA cloning and biochemical characterization of s-adenosyl-L-methionine: 2,7,4'-trihydroxyisoflavanone 4'-o-methyltransferase, a critical enzyme of the legume isoflavonoid phytoalexin pathway
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product="S-adenosyl-L-methionine: daidzein
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Pred. No. 3.2e-148;
0; Mismatches 197;
                                                                                            Plant Cell Physiol, 44 (2), 103-112 (2003) 22497945
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/mol_type="mRNA"
/db_xref="taxon:46348"
/cell_line="Ak-1"
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48. .1121
/gene="D7OMT"
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80.1%;
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AAGAGAGAAAAGAAGATTGGAAGAACTCTTCATGGAAGCAGGGTTCCAAAGCTACA 1037
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Medicago sativa
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
Medicago.
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   GGGACATGTTTAAATGCATCCCCAAGGCTGATGCAGTTCTGCTTAAGTTGGTTTTACATA
                                                                                                  ATTGGACTGATAAGGATTGCCTAAGGATACTGAAGAATGTAAAGAAGCTGTTACAAATG
                                                                                                                                        AAAGCAAAACAGGAAAAGTAGTTGTCATAGATACTGTGATAAACGAAAAAAAGATGAGC
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                                GGGACATGTTCACATCTACTACTGCTGATGCAGTTTTGCTTAAGTATATTCTACATA
                                                                     ATTGGAATGACGATTGCATGAAGATATTAGAAAATTGTAAAGAAGCTATTTCAGGTG
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Dixon,R.A. and He,X.Z.
Isoflavonoid methylation enzyme
Patent: WO 0011736-A 1 30-NOV-2000;
The Samuel Roberts Noble Foundation,
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Sequence 1 from Patent W00071736.
AX050436
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NTSNDAMASDSKLINLALRDCDFVFDGLESIVDVGGGTGTTAKIIGETFPKLKCIVF
DR.PQVVBNLSGSNNITYVGGDNGTSIPNADAVLLKYTILLKKCKEAVY
NDGKRGKVITIDMVIDEKKDENQVTQIKLLMDVNMACLNGKERNEEEWKKLFIEAGFQ
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                                                                                                                                                                                                                                                                                                                                                                     Length 1284;
                                                                                                                                                                                                                                                                                                                                                                     Score 647; DB 8; I
Pred. No. 1.1e-136;
0; Mismatches 250;
                                                                                                                        /codon_start=1
/product="7-0-methyltransferase"
 organism="Medicago sativa"
                    type="mRNA"
xref="taxon:3879"
                                                                                                                                                                                                                                                                                                    HYKISPLTGFLSLIEIYP"
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                                                               /gene="7-IOMT(6)"
30. .1088
                                                                                                        gene="7-IOMT(6)"
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76.1%;
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2 Stress responses in alfalfa (Medicago sativa L). XXII. cDNA cloning and characterization of an elicitor-inducible isoflavone
1 O-methyltransferase
1 Plant Mol. Biol. 36 (1), 43-54 (1998)
2 P44461
2 States 1 to 1231)
2 (bases 1 to 1231)
2 (bases 1 to 1231)
3 He,X., Reddy,J.T. and Dixon,R.A.
5 Direct Submission
1 Submitted (11-APR-1997) Plant Biology Division, The Samuel Roberts
Noble Foundation Inc., 2510 Sam Noble Parkway, Ardmore, OK 73401, USA
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IQNHGKPISLSNLVSILQVPSSKIGNVRRLMRYLAHNGFFEIITKEEESYALTVASEL
LVRGSDLCABAVBCVLDPTLSGSYHBLKKMYTREDDTLFGTVTLGSCFWDFLDRNPBY
NTSFNDAMASDSKLINLALTDCDFVEDGLSSIVDVGGGTGTVAKIGCFFFKLKCIVF
DRPQVVBNLGSGNNLTYVGGDMFTSIPNADAYLLKYILHNWTDKDCLRILKKCYEAVT
NDGKRGKVTIIDMVIDKKKDBNQYTQIKLLMDVNMACLNGKERNEEEWKKLFIEAGFQ
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae,
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/product="isoflavone-O-methytransferase"
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/note="7-IOMT; 7-0-methyltransferase"
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Pred. No. 2.6e-136;
0; Mismatches 251;
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/db_xref="GI:2580540"
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/db_xref="taxon:3879"
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/organism="Medicago
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Matches 841
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He,X.Z., Reddy,J.T. and Dixon,R.A.
Stress responses in alfalfa (Medicago sativa L). XXII. cDNA cloning and characterization of an elicitor-inducible isoflavone
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Direct Submission
Submitted (23-APR-1997) Plant Biology Divsion, The Samuel Roberts
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1 (bases 1 to 1194)

2 CDNA of an additional member of the isoflavone-O-methyltransferase (IOMT2) gene family in Medicago sativa (Accession No. AF023481) (PGR97-170)

2 (bases 1 to 115, 1289 (1997)

2 (bases 1 to 1194)

He,X.Z. and Dixon,R.A.
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protein_id="AAB88294.1"
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/mol_type="mRNA"
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400 418 460 475 520 529 580 583

649 700 709 760 769 820 829 889

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                                                                                                               AACAATGGCCGTAAAGCAAGTGAGATTTTTCAAGGTCAAGCTCTTTTTGTACAATTTG
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IHNHGKPITLPBLASALKLHPSKVGILYRFLKLLTHNGFPAKTTVPSQNGKDGBEBEB
TAYALTPPSKLLVKGKPFTCASIVRGALHPSSLDWMRSSEKWFKEDKBLTLFRSATGB
THVPLNKSKEJSNEQEAMADSQMFKLALKECRHVFBGIESLVDVGGGTGGYTK
LIHBEPPHLKCTVFDGDQVVGNLSGNBNLKFVGGDMFKSIPPADAVLLKWVLHDWNDE
LSLKILKNSKBAISGKCKEGKVIIIDISIDEASCORBETFELQLDYDLVWTTMFNGKER
EKKEWEKLISDAGFSSYKITFICGFKSLIEVFP"
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Glycyrrhiza echinata
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Galegeae;
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Assah.T. Aoki.T. and Ayabe,S.

Direct Submission
Submitted (14-SBP-2002) Shin-ichi Ayabe, Nihon University,
Department of Applied Biological Sciences; Kameino 1866, Fujisawa,
Kanagawa 252-8510, Japan (B-mail:ayabe@brs.nihon-u.ac.jp,
Tel:81-466-84-3703, Pax.81-466-80-1141)
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ALCAAGTTACTCAAATTAAGCTCCTTATGGATGTAAACATGGCTTG---TCTAAATGGAA
                                                                                                     AAGAGAGAAAAAGAAGATTGGAAGAAACTCTTCATGGAAGCAGGGTTCCAAAGCTACA
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/protein id="BAC58011.1"
/db_xref="G1:28804592"
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/note="cloning vector: lambda ZapII~cultured cells"
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/product="S-adenosyl-L-methionine:
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      CACAGCCATAGCCATGGCCAACCCATTACTTTTCAGAGTTGGTGTCAATTCTACAAGTC
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                                                                                     209 CCACCAACTAAAACTCGTCAGGGCCTCATGCGTTATCTAGCACACAATGGATTC
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    -AAGAICTCACAGTAITTGAGGTCTCCTTAGGAACACCTTTCTGGGGACTTTATCAATAAA

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AC136140.8 GI:31455653
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IHNHGKPMTLPELSSSLKLHPSKVNILYRFLRLLTHNGFFAKTTVKSNEGEEETAYVL
TPSSKLLVSGKSTCLSSLVKGALHPSSLDMWGVSKKWFHEDKEQTLFECATGENYWDF
LNKDSDSLSNFODAMAADSRLFKLAIQENKHVPEGLESLVDVAGGTGGVAKLIHEAFP
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NSKBAISHKGKDGKVIIDISIDBNSDDRGLTELQLEYDVVMLTMFLGKERTKKEWEK
LIYDAGREYNITPICGFKSLIEVYP*
204 c 266 g 417 t
ATAICCGACGCAGGGIICAGCAGCIACAAGAIIACCCCCAIIIGIGGCIICAAGICCCIC 1120
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W.Q., Presisty, C.L. and VanEtten, H.D.
Isolation of the cDNAs encoding (+) 6a-hydroxymaackiain
3-O-methyltransferase, the terminal step for the synthesis of the phytoalexin pisatin in Pisum sativum
Plant Mol. Biol. 35 (5), 551-560 (1997)
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                                                                                                                                                                                                         (hmm6) mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           University of Arizona, 21. USA
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/hote="methyltransferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="6a-hydroxymaackiain methyltransferase"
/protein_id="AAC49856.1"
/db_xref="GI:1568637"
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Pisum sativum 6a-hydroxymaackiain methyltransferase
U69554
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Wu,Q., Preisig,C.L. and VanEtten,H.D.
Direct Submission
Submitted (04-SEP-1996) Plant Pathology, Univ
Forbes Building, Room 204, Tucson, AZ 85721,
Location/Qualifiers
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/function="pisatin biosynthesis;
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Pred. No. 1.1e-62;
0; Mismatches 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Pisum sativum"
/mol_type="mRNA"
strain="Alaska"
/db_xxef="taxon:3888"
                                                                                  ATTGAAGTTTTTCCTTAATT 1140
                                          ATTGAGATCTATCCTTGAAT 1089
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FEATURES

207 TCCCACCAACTAAAACTCGTCAGGTGCAGAGCCTCATGCGTTATCTAGCACACAATGGAT 266	Db 104372 TCTTCGCAATTGTGAAGATAGACGACAACAAAGGAGCATATGCTCTTTCTCCAACAACAA 104313 QY 327 AGTTACTTGTCAAAAGCAGTGAGCTTAGTTTTAGCTCCAATGGTTGAGTATTTTCTTGAAC 386 Db 104312 AGCTTCTTGTAAAAGAACTGATCATTATTTTCAATGCTTAAGTTGCTAACAAACC 104253	387 CAAATTGTCAAGGTGCATGGAACCAGTTGAAGAGGTGGGGTTCATGAGGAAGATCTCACAGGAGTGGAGATCTCACAGGGTGGGGTTCATGAGGAAGATCTCACAGGACAGGAGATACCAATTGAAGCACTGGACATCAATGGAGGACCTCACAA	104192	Db 104144 CCAAGTTATTCAATGATGGTATGGAAAGTGATTCTAATATGGTGAGGTTTGCAATGAGTG 104085 OY 567 ATTGCAATTGGGTCTTTGAGGGACTGGAATCCATTGTGGATGTTGGTGGTGGAACTGGAA 626 Db 104084 ATTGCAAATCAGTTTTTGAGGGCTTAACTTGGTTGATGTTGGAGGTGAACCGAA 104025	OY 627 TCACAGCAAAGATTATCTGTGAGGCTTTTCCTAAGCTGAAATGCATGGTGTTGGAACGTC 686 Db 104024 ACACTGTTAAAATTATTTGTGAGGCGTTTCCTACGTTAAAATGTATAGTGTTCGACTTT 103965	OY 687 CAAATGITGIGGAAAAITIGICAGGAAGCAACAAITIGACAITIGIGGGGGGACAIGI 746 Db 103964 CAAACGIGGIAGAAGGAITAACGGGAAAIAACTAICIGAGITITGIAGGCGGAAACAIGI 103905	747 TTAAATGCATCCCCAAGGCTGATGCAGTTCTGCTTA	OY /83		863 AAAACAGGAAAAGTAGTTGTCATAGATACTGTGATAAACGAAAACAAAGGCCCAA 103664 AAAGAAAAAGTGATCATAATACATATTGTGATAAATGAAGAGAAGATGAGCCCAA		103		RESULT 10 AB091686 LOCUS AB091686 1363 bp mRNA linear PLN 04-MAR-2003 DBFINITION Lotus japonicus H14'OMT mRNA for S-adenosyl-L-methionine:
ttula (barrel medic) ttula tiplantae, Streptophyta; Embryophyta; Tracheophyta; Magnoliophyta; eudicotyledons; core eudicots; Is I; Pabales; Pabaceae; Papilionoideae; Trifolieae;	<pre>1 (Dases 1 to 111587) Shault,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B., Cook,D., Kim,D. and Roe,B.A. Medicago truncatula BAC Clone mth2-11a20 Unpublished 2 (Dases 1 to 111587)</pre>	Shaull,S., Lin,S., Dixon,R., May,G., Sumher,L., Gonzales,B., COOK,D., Kim,D. and Roe,B.A. Direct Submission Submitted (29-007-2002) Department Of Chemistry And Biochemistry, The University Of Oklahoma. 620 Parrington Oyal Room 208 Morman	Sumner, L., Gonzales, B.,	The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA On this sequence version replaced gi:30061413.		consists of 3 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have	זק	* 9682 9781: gap of unknown length * 9782 46738: contig of 36957 bp in length * 46739 46838: gap of unknown length * 46839 111587: contig of 64749 bp in length.	truncatula" NA"	/clone_lib="Medicago truncatula BAC library H2" //note="This is one of two clones in the same well from mth2-lla20" BASE COUNT 37516 a 18138 c 18553 g 37160 t 220 others ORIGIN	Query Match 27.5%; Score 318.8; DB 2; Length 111587; Best Local Similarity 58.8%; Pred. No. 2.78-62; Matches 699; Conservative 0; Mismatches 347; Indels 142; Gaps 3;	27 ACAATGGCCGTAAAGCAAGTGACATTTTCAAGGTCAAGCTCTCTTGTACAAACATTTGC 86	0/ 1195011CHAMAILLIAMAGIGICHAAANIGGTIGACATACCCGACATAA 146 	OY 147 TCCACAGCCATGGCCAACCCATTACTTTTCAGAGTTGGTGTCAATTCTACAG 206 Db 104486 TTCAAATCATGGCAACCTATTACTCTTCCGAGCTTGTCTGGCTCTTCGAA 104433 Db 104486 TTCAAATCATGGCAACCTATTACTCTTCCCGAGCTTGTCTGGAA 104433

VERSION KEYWORDS

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                                                GACATACCCGACATAATCCACAGCCATAGCCATGGCCAACCCATTACTTTTCAGAGTTG
                                                                                         174 GGCATCGCCGACGTGATCCAC----AGCCATGGAAAACCCATCACCTCCCTGAGTTA
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VIKSHGKPITLEELATALNLRESKIGVLHRFIRLLITHGFFAKTTVSRGEGAEEETAY
GLTPFSKLLVKSNSTCLAPIVKGALHRFIRLLITHGFFAKTTVSRGEGAEEETAY
GLTPFSKLLVKSNSTCLAPIVKGALHPSSLDMRRSSKWFELBDREETTELEBJATGRSF
WEFLNKETESDTLAMPQBAAAADSHMFKLALKECKHYPEGLGSLVDVAGGRGGGVTKLI
KRITSCTVRDQPQVYANLTGDENLNFVGGDMFKSVPPADAVLLKWVLHDWNDELS
LKILKNCKEAISGRGKECKVIIIDISIDETSDDRELTELKLDYDLVMLTMFNGKEREK
KEWEKLIYDAGGSYKITPICGRKSLLEVFP"

288 G
368 L
      cds.
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Masshir. Aokir. and Ayabe, S.
Direct Submission
Submitted (14-SEP-2002) Shin-ichi Ayabe, Nihon University,
Department of Applied Biological Sciences; Kameino 1866, Fujisawa,
Kanagawa 252-8510, Uapan (E-mail:ayabe@brs.nihon-u.ac.jp,
Tel:81-466-84-3703, Fax:81-466-80-1141)
Location/Qualifiers
                                                                                                       Lotus japonicus
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
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2,7,4'-trihydroxyisoflavanone 4'-O-methyltransferase, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Almost identical to entire nucleotide sequence AV407445."
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/protein_id="BAC58013.1"
/db_xref="G1:28804596"
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                                                                                                                                                                                                                                    Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
Generation of 7137 non-redundant expressed sequence tags
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s-adenosyl-L-methionine: 2,7,4'-trihydroxyisofla
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Plant Cell Physiol. 44 (2), 103-112 (2003)
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/strain="MG-20 Miyakojima"
/db_xref="taxon:34305"
                                                                                                                                                                                                                                                                       legume, Lotus japonicus
DNA Res. 7 (2), 127-130 (2000)
20277479
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Lavid, N., Wang, J., Shalit, M., Guterman, I., Bar, E., Beuerle, T., Menda, N., Shafir, S., Zamir, D., Adam, Z., Vainstein, A., Weiss, D., Pichersky, E. and Lewinsohn, E.
                                                                                                                                                         447' IGGGATGACATGTTGGGATTATGTGAACCAGGACCCGACTCTTGCACTTTTTTCAATGA
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O-methyltransferases involved in the biosynthesis of volatile phenolic derivatives in rose petals
Plant Physiol. 129 (4), 1899-1907 (2002)
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1 (base; lto 1257)

Mbeguie-A-Mbeguie, D., Gomez, R.-M. and Fils-Lycaon, B.
Sequence of an O-Methyltransferase from Apricot Fruit (Accession No. U82011). Gene Expression During Fruit Ripening (PGR97-118)

L. Plant Physiol. 114, 1569 (1997)

E. Chases I to 1257

Mbeguie A Mbeguie, D., Gomez, R.-M. and Fils-Lycaon, B.
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LDLPHVVADLKGSKULSYVAGNPFRAYPADAIFLKMILHDWSDESCVKILERCKAAV
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fissue_type="fult mesocarp and of
dev_stage="ripe"
10. ..1074
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                                      Prunus armeniaca methyltransferase mRNA,
mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Prunus armeniaca"
/mol_type="mRNA"
/strain="Bergeron"
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/product="methyltransferase"
/protein_id="AAB71213.1"
/db_xref="GI:2282586"
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I. Rosales, Rosaceae, Rosoideae, Rosa.
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Characterisation of a novel O-methyltransferase involved in the blosynthesis of 3,5-dimethoxytoluene and 1,3,5-trimethoxybenzene, two major scent components of rose flowers
                                      GATGATTCCAAAGGAGTGTTTGAGGGATTAGAGTCATTGGTCGATGTTGGTGGTGGTACA
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    -GAGATTGCAATTGGGTCTTTGAGGGACTGGAATCCATTGTGGATGTTGGTGGTGGAACT
                                                                                          GGAATCACAGCAAAGATTATCTGTGAGGCTTTTCCTAAGCTGAAATGCATGGTGTTGGAA
                                                                                                                                  GGAACTGTGGCAAAGGCTATTGCTGATGCATTCCCACATATTGAATGCACTGTACTTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    884 AAGAAAGGCAAGGTGATTATCATAGATGATGATGGAGGAACCAGAAGGGGGGATGAGGAAA
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/product="orcinol O-methyltransferase"
/protein_id="CAD29459.1"
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Rosa chinensis
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/mol_type="mRNA"
/cultivar="01d Blush"
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Submitted (25-MAR-2002) RDP,
07 69364, France
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Cock, J.Mark.
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TFWDYGNHQPSIAHLFNDAMASDARLVTSVIIDDCKGVFEGLESLVDVGGGTGTVAKA
ITADAPPHIECTVLDLHHVVADLGGSKNLKYTGGDMFRAVPPADTVLLKWILHDWNDSE
CIKLIKRSRVAITSKDKKGKVIIDMMENQKGDEESIETQLFFDMLMMALVRGGERN
EKEWAKLFTDAGFSVXITPLIGGRELIEVYF"
270 c 255 g 329 t
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/brotein_id="G1:20514359"

/translation="TRELNORWSNGEHSNELLHAQAHIWNHIPSFINSMSLK

SAIQLGIPDIINKHGPMTLSELFSALPIHPTKGHSVYRLARILVHSGFPAKKKLSKTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88
                    Submitted (15-APR-2002) Vegetables Crops, Newe Ya'ar Research Center, Agricultural Research Organization, P.O. Box 1021, Ramat Yishay 30095, Israel Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                             /function="catalyzes the S-adenosylmethionine-dependent O-methylation of 3-methoxy, 5 hydroxytoluene to form 3,5-dimethoxytoluene (orcinol dimethyl ether)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATGGAGAGCATTCCAACGAGCTACTTCATGCTCAAGCCCACATCTGGAACCACATCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 AGCTTCATAAACTCCATGTCCCTCAAATCTGCAATTCAACTAGGTATACCAGATATCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATGGCCGTAAAGCAAGTGAGATTTTTCAAGGTCAAGCTCTCTTGTACAAACATTTGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89 GGCTTCATAGATTCTAAGTGTCTAAAATGGATGGTTGAGCTTGACATACCCGACATAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CACAGCCATAGCCATGGCCAACCCATTACTTTTCAGAGTTGGTGTCAATTCTACAAGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCACCAACTAAAACTCGTCAGGTGCAGGCCTCATGCGTTATCTAGCACACAATGGATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          446 GIAITIGAGGICTCCTTAGGAACACCTTTCTGGGACTTTATCAATAAAGACCCTGCATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACAAGTCATTCAATGAGGCAATGGCTTGTGATTCTCAGATGTTGAACTTGGCGTTTA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       464 CCATITGACACAGGACATGGGATGACATITTGGGATTACGGGAACCATCAGCCAAGTATT
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                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/product="orcinol O-methyltransferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 302.8; DB 8;
Pred. No. 2.1e-58;
); Mismatches 442;
                                                                                                                         /organism="Rosa hybrid cultivar"
/mol_type="mRNA"
/cultivar="Fragrant Cloud"
/isolate="fc0895"
/db_xref="taxon:128735"
                                                                                                                                                                                                                                       type="petals"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                           'gene="00MT2"
                                                                                                                                                                                                                                                                                  gene="OOMT2"
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TCAATTGAAACGCAGCTGTTCTTCGACATGCTGATGACGCCCTCGTCAGAGGACAAGAA 1015
                                                                                                                                                                                              1016 AGGAATGAGAAAGAATGGGCTAAGCTCTTCACTGATGCTGGTTTCAGTGACTATAAGATA 1075
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AIADAFPHIECTVLDLPHVVADLQGSKNLKYTGGDMFEAVPPADTVLLKWILHDWSDE
ECIKILERSRVAITGKEKKGKVIIIDMMMENQKGDEESIETQLFFDMLMMALVGGKER
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protein_id="aAM23004.1"
|db_xref="GI:20514367"
|translation="MBRLNSFRHLNOKWSNGEHSNELLHAQAHIWNHIFSFINSMSLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAIQLGIPDIINKHGYPMTLSELTSALPIHPTKSHSVYRLMRILVHSGFFAKKKLSKT
DEEGYTLITDASQLLLKDHPLSLTPYLTAMLDPVLTNPWNYLSTWFQNDDPTPPDTAHG
                                                       Rosa hybrid cultivar
Rosa hybrid cultivar
Rosa hybrid cultivar
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; eudicotyledons; core eudicots;
rosids; eurosids 1; Rosales; Rosaceae; Rosaidese; Rosa.
       896 AAGAAAGGCAAGGTGATTATCATAGATATGATGGAGAACCAGAAGGGGGATGAGGAA 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (15-APR-2002) Vegetables Crops, Newe Ya'ar Research Center, Agricultural Research Organization, P.O. Box 1021, Ramat Yishay 30095, Israel Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /function="catalyzes the S-adenosylmethionine-dependent O-methylation of orcinol (3.5-dihydroxytoluene) to form 3-methoxy, 5 hydroxytoluene" /codon_start=1
                                                                                                                                                        AGAAAAGAAGAAGATTGGAAGAACTCTTCATGGAAGCAGGGTTCCAAAGCTACAAAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l (bases I to 122).
Lavid,N., Wang,J., Shalit,M., Guterman,I., Bar,E., Beuerle,T., Mend,N., Mang,J., Shalit,M., Guterman,I., Bar,E., Beuerle,T., Menda,N., Shafir,S., Zamir,D., Adam,Z., Vainstein,A., Weiss,D., Pichersky,E. and Lewinsohn,E.
O-methyltransferases involved in the biosynthesis of volatile phenolic derivatives in rose petals
Plant Physiol. 129 (4), 1899-1907 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 1252)
Lavid,N., Wang,J., Shalit,M., Guterman,I., Bar,E., Beuerle,T.,
Menda,N., Shafir,S., Zamir,D., Adam,Z., Vainstein,A., Weiss,D.,
Pichersky,E. and Lewinsohn,E.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                         1252 bp mRNA linear PLN 14-AUG cultivar orcinol O-methyltransferase (OOMI) mRNA,
                                                                                                                                                                                                                                                                                          1076 ACTCCCATTTTGGGTTTAAGGTCTCTTTGAGGTTTTATCCTTGATAATT 1125
                                                                                                                                                                                                                                                    1043 TCTCCCTTCACAGGATATTTGTCTCTTATTGAGATCTATCCTTGAATACT 1092
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/organism="Rosa hybrid cultivar"
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/cultivar="Fragrant Cloud"
/isolate="fc0496"
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1. .1252
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                      /translation="MERLNSFKHINOKWSNGEHSNELLHAQAHIWNHIFSFINSMSLK
SAQLGTBDINKHGPWTLSELTSBLTDALDPHPTKBBYVELMRITUHSGFRKKKLSKTD
SEGYTLTDASQLLLLSELTSFLTAKLDPFULTTPMNYLLSTRFQNEDPTPFTAHGM
TFWDYGNHQPSIAHLENDAMASDARLVTSVIIDDCKGVPEGLESLVDVGGGTGTVAKGM
TFWDYGNHQPSIAHLENDAMASDARLVTSVIIDDCKGVPEGLESLVDVGGGTGTVAKG
TADAPPHIISCYVLDLPHYVADLGGSKVLKTTGGDMFBAVPPADTVLLKWILHGWNDEE
CIKLIKKSRNALTSCRKKYIIIDMWNENQKGDEESIETQLFFDMLMYALLVGGERN
EKEWAKLFTDAGFSDYKIIPILGLRSLIEVYP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCTTCATAGATTCTAAGTGTCTAAAATGGATGGTTGAGCTTGACATACCCGACATAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 AGCTTCATAAACTCCATGTCCCTCAAATCTGCAATTCAACTAGGTATACCAGATATCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CACAGCCATAGCCATGGCCAACCCATTACTTTTCAGAGTTGGTGTCAATTCTACAAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 AACAAACATGGC-----CCCATGACTCTTTCTGAGCTCACATCTGCACTACCAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCACCAACTAAAACTCGTCAGGTGCAGAGCCTCATGCGTTATCTAGCACACAATGGATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITGAGATAGTAAGAATCCATGACA - - - ACATAGAAGCATATGCTCTCACTGCTGCTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Triccraagaaaaagcraagaaarcraargaagaaagcrraracccrracraargcrrcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGCTCCTTCTGAAGGATCATCCCTTAAGCCTAACGCCCTTCTTAACCGCCCATGCTCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCAAATTGTCAAGGTGCATGGAACCAGTTGAAGAGGTGGGTTCATGAGGAAGATCTCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTATTTGAGGTCTCCTTAGGAACACCTTTCTGGGACTTTATCAATAAAGACCCTGCATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         536 GCCCATTTGTTCAATGATGCCATGGCTAGCGATGCTCGGTTGGTCACCAGCGTGATCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -GAGATTGCAATTGGGTCTTTGAGGGACTGGAATCCATTGTGGATGTTGGTGGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       596 GATGATTGCAAAGGAGTGTTTGAGGGATTAGAGTCATTGGTCGATGTTGGAGGTGGTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAATCACAGCAAAGATTATCTGTGAGGCTTTTCCTAAGCTGAAATGCATGGTGTTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGTCCAAATGTTGTGGAAAATTTGTCAGGAAGCAACAATTTGACATTTGGTGGGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCCCACATGTGGTGGCTGACCTGCAAGGAAGTAAGAACTTGAAATATACTGGAGGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 743 AIGITIAAAIGCAICCCCAAGGCIGAIGCAGIICIGCTIAAGIIGGIITIIACAIAAIIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arcrirgaggcagriccrccrcccaracacrirracrcaagragararrecarge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  803 AATGACAACGATTGCATGAAGATATTAGAAAATTGTAAAGAAGCTATTTCAGGTGAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  476 CCATTTGACACAGCACATGGGATGACATTTTGGGATTACGGGAACCATCAGCCAAGTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         506 AACAAGICATICAAIGAGGCAAIGGCTIGIGATICICAGAIGTIGAACIIGGCGITIA--
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                        15;
                                                                                                                                                                                                                                                                        Length 1265;
                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                     26.1%; Score 302.8; DB 8; ilarity 57.3%; Pred. No. 2.1e-58; Conservative 0; Mismatches 442;
db xref="GI:27527924"
                                                                                                                                                                                              265 g
                                                                                                                                                                                                 273 c
                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                     Query Match
Best Local Simi
Matches 613;
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/gene="comt1"
/codon_start=1
/codon_start=1
/product="rocinol 0-methyltransferase"
/protein_id="c0b29458.1"
/protein_id="c0b29458.1"
/db_xref="G1:27527922"
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/translation="MBRLNSFRINGWSNGBHSNELLHAQAHIWNHIFSFINSMSLK
SAIQLGIPDIINKHGYPWTLAELTSALPIHFTKSHSYVRLMRILVHSGFFAKKLSKT
DBEGYTLTDASQLLLKOHPLSLTPYLTAMLDPVLTNPWNYLSTWFQNDDPTPFDTAHG
MTRWDGWARGPSTARLENDAMASDARLAYTSVIINGKGYPTSESLLVVGGGTGTTLAK
AIADAFPHIBCTVLDLEPHVVADLQGSKNLKYTGGDMFBAYPPADTVLLKVILLKVILLKVILLKVILLKGGTGFE
BCIKILERSRVAITGKEKKGKVIIIDMMENQKGDESIETQLFPPDMLMMALVGGKER
                                                                                                                                                                                                         PLN 06-JAN-2003 (comt1 gene).
                                                                                                                                                                                                                                                                                                                                                                     Rosa chinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids 1; Rosales; Rosaceae; Rosoideae; Rosa.
1 (bases 1 to 1275)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 ITTGAGATAGTAAGAATCCATGACA---ACATAGAAGCATATGCTCTCACTGCTGCTTCA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lyon cedex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cock, J.Mark., Scalliet, G. and Hugueney, P. Characterisation of a novel O-methyltransferase involved in the biosynthesis of 3,5-dimethoxytoluene and 1,3,5-trimethoxybenzene, two major scent components of rose flowers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATGGAGAGCATTCCAACGAGCTACTTCATGCTCAAGCCCACATCTGGAACCACATCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89 GGCTTCATAGATTCTAAGTGTCTAAAATGGATGGTTGAGCTTGACATACCCGGACATAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 AGCTTCATAAACTCCATGTCCCTCAAATCTGCAATTCAACTAGGTATACCAGATATCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 AACAAA-----CATGGTTACCCCATGACTCTTTCTGAGCTCACATCTGCACTACCAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCACCAACTAAAACTCGTCAGGTGCAGAGCCTCATGCGTTATCTAGCACACAATGGATTC
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                                             ACTCCCATTTCGGGTTTAAGGTCTCATTGAGGTTTATCCTTGATATT
   TCTCCCTTCACAGGATATTTGTCTCTTATTGAGATCTATCCTTGAATACT
                                                                                                                                                                                                      mRNA linear
O-methyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 302.4; DB 8;
Pred. No. 2.5e-58;
0; Mismatches '446;
                                                                                                                                                                                                                                                                                                                  oomt1 gene; orcinol O-methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46,
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/organism="Rosa chinensis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENSI,
                                                                                                                                                                                             Rosa chinensis mRNA for orcinol AJ439741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:74649"
1. .1275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/cultivar="Old Blush"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                iocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              266 g
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Submitted (25-MAR-2002)
07 69364, France
                                                                                                                                                                                                                                                                                       GI:27527921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="oomt1"
20. .1123
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llarity 57.2%;
Conservative
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Cock, J.Mark.
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                                                                                                                                                                                                                                                                                                                                                   Rosa chinensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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Best Local Simi
Matches 612;
   1043
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SOURCE
ORGANISM
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ORIGIN
                                                                                                                                             RESULT 15
RCH439741
                                                                                                                                                                                                                                                         ACCESSION
VERSION
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AUTHORS
TITLE
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AUTHORS
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JOURNAL
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                                                                                 ω,
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Medicago sativa ca Alfalfa COMT clone Arabidopsis thalia

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AAX26295 ABX28928

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AAC42978 ABZ14777

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L. styraciflua ang Eucalyptus grandis cDNA encoding (iso

AAD11127 AAA68014

AAV71042

AAD47178 AAA68081

AAZ88734

Clarkia breweri IE Eucalyptus grandis P. sylvestris PMT

ALIGNMENTS

Falco SC;

Fader GM,

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Isoflavone O-methyltransferase, soybean, degradation, daidzein, Flavonoid, flower colour, growth, pollination, irradiation, ss.
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/*tag= // Product= Isoflavone_O-methyltransferase
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(S)-3'-hydroxy-N-m
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7316.234 Million cell updates/sec
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                                                                                                                    2003, 23:29:44 ; Search time 428 Seconds
               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Genetically manipulating biologically active 4'-O-methylated isoflavonoid for producing plants with increased disease resistance, and for accumulation of 4'-O-methylated isoflavonoid nutraceuticals in
       GCTGAAATGCATGGTGTTGGAACGTCCAAATGTTGTGGAAAATTTTGTCAGGAAGCAACAA
                                                                                                                                               TAAGTTGGTTTTTACATAATTGGAATGACAACGATTGCATGAAGATATTAGAAAATTGTAA
                                                                                                                                                                                   AGAAGCTATTTCAGGTGAAAGCAAAACAGGAAAAGTAGTTGTCATAGATACTGTGATAAA
                                                                                                                                                                                                                 AGAAGCTATTTCAGGTGAAAGCAAAACAGGAAAAGTAGTTGTCATAGATACTGTGATAAA
                                                                                                                                                                                                                                                                                                                                                                  Alfalfa; isoflavone 4'-O-methyl transferase 8; IOMT; transgenic plant;
                                                                             TTTGACATTTGTTGGTGGGGACATGTTTAAATGCATCCCCAAGGCTGATGCAGTTCTGCT
                                                                                                                                                                                                                                                          CGAAAACAAAGATGAGCGCCAAGTTACTGAACTAAAGCTCCTTATGGATGTACACATGGC
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                                         TTTGACATTTGTTGGTGGGGACATGTTTAAATGCATCCCCAAGGCTGATGCAGTTCTGCT
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                                                                                                                                                      were prepared from soybean embryo (19 days after flowering), root, 8-day old root and seed (25 days after flowering).

Isoflavone onethyltransferase catalyses the first step in degradation of daidzein. Suppression of this enzyme will yield higher concentrations of this beneficial isoflavone in, e.g. soybean seed. Flavonoids serve as co-pigments in flower colour, stimulate pollen tube growth, attract pollenators, act as feeding deterrents and protect against UV irradiation in fruits and seeds. The cDNA and proteins can be used to isolate homologues, for immunological screening and for positive
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Pred. No. 3.4e-295;
Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                             Sequence 1160 BP; 361 A; 197 C; 254 G; 348 T; 0 other;
                                                                                                         2; Page 32; 39pp; English
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2000-442680/38
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coding sequence from Alfalfa. The present invention relates to a method for genetically manipulating the level of biologically active IOMT. The method involves transforming the target plant with a DNA fragment (the present sequence) to form a transgenic plant. IOMT is useful as foodstuff, nutritional supplement, animal feed supplement, nutraceutical and as a pharmaceutical. Transgenic expression of IOMT in lequmes is useful for engineering both phytoalexin levels for improved disease resistance, and health promoting nutraceutical phytochemicals. IOMT is useful for engineering isoflavone 4'-O-methylation, or other organisms.
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                                                                                                                                                                                                                                                                                          CTTCATTAAACAATGGCCGTAAAGCAAGTGAGATTTTTCAAGGTCAAGC
                                                                                                                                                                                                                      Score 645.4; DB 22; Length
Pred. No. 9.7e-160;
0; Mismatches 251; Indels
                                                                                                                                                                                      Sequence 1231 BP; 402 A; 183 C; 235 G; 411 T; 0 other;
                                                                                                                                                         naturally produce isoflavonoids.
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Isoflavone O-methyltransferase catalyses the first step in degradation of daldzein. Suppression of this enzyme will yield higher concentrations of this beneficial isoflavone in, e.g. soybean seed. Flavonoids serve as co-pigments in flower colour, stimulate pollen tube growth, attract pollenators, act as feeding deterrents and protect against UV irradiation in fruits and seeds. The CDNA and proteins can be used to isolate homologues, for immunological screening and for positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA29321-25 encode isoflavone O-methyltransferases isolated from various soybean (Glycine max) tissues. CDNA libraries se4, sr1, srr1c and ss11c were prepared from soybean embryo (9) days after flowering), root, 8-day old root and seed (25 days after flowering).
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                                                                                                                                                                                                917 ATCAAGTTACTCAAATTAAGCTCCTTATGGATGTAAACATGGCTTG---TCTAAATGGAA
858 AAAGCAAAACAGGAAAAGTAGTTGTCATAGATACTGTGATAAACGAAAACAAAGATGAGC
                                                                      AAGAGAGAAAAAAGATTGGAAGAACTCTTCATGGAAGCAGGGTTCCAAAGCTACA
                                                                                                                                                                                                                                                                                                                                                                         974 AAGAGAGAAATGAGGAAGAATGGAAGAACTCTTCATAGAAGCTGGTTTCCAACACTATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAATATCTCCCTTCACAGGATATTTGTCTCTTATTGAGATCTATCCTTGAATACTGACGC
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                                                                                                                                                         918 GCCAAGTTACTGAACTAAAGCTCCTTATGGATGTACACACATGGCATGTATTAATGGAA
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transgenic plants and for immunological screening of cDNA libraries
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flower colour; growth; pollination; irradiation; ss
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AMA29321-25 encode isoflavone O-methyltransferases isolated from various soybean (Glycine max) tissues. CDNA libraries se4, sr1, srr1c and ssl1c were prepared from soybean embryo (19 days after flowering), root, 8-day old root and seed (25 days after flowering).

Isoflavone O-methyltransferase catalyses the first step in degradation of daidzein. Suppression of this enzyme will yield higher concentrations of this beneficial isoflavone in, e.g. soybean seed. Flavoncids serve as co-pigments in flower colour, stimulate pollen tube growth, attract pollenators, act as feeding deterrents and protect against UV irradiation in fruits and seeds. The cDNA and proteins can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 CATTAAACAATGGCCGTAAAGCAAGTGAGATTTTTCAAGGTCAAGCTCTCTTGTACAAAC 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide encoding flavonoid biosynthetic enzymes for creating transgenic plants and for immunological screening of cDNA libraries
                                                           1051 CACAGGATATTTGTCTTTATTGAGATCTTATTCGTTGAATACTGACGCTGCAATATTCCAT
                                                                                              1012 CTTTGGTTTCAGATCTCTAATTGAGCTCTATCCTTAGACATATATCCTAGCTTGTATGC
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                                                                                                                                                                                                                                                                                                                                                                                                 Glycine max isoflavone O-methyltransferase clone srr1c.pk001.b16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isolate homologues, for immunological screening and for positive selection methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                    O-methyltransferase; soybean; degradation; daidzein; flower colour; growth; pollination; irradiation; ss.
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Pred. No. 2.2e-123;
0; Mismatches 318; Indels
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/transl except= (pos:268..279, aa:Glu)
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                                                                          Score 508.6; DB 21; Length 1253;
Pred. No. 1e-123;
); Mismatches 339; Indels 12;
                                       Sequence 1253 BP; 374 A; 232 C; 267 G; 380 T; 0 other;
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larity 68.2%;
Conservative
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Isoflavone O-methyltransferase catalyses the first step in degradation of daidzein. Suppression of this enzyme will yield higher concentrations of this beneficial isoflavone in, e.g. soybean seed. Plavonoids serve as coligments in flower colour, stimulate pollen tube growth, attract pollenators, act as feeding deterrents and proteins can be used to irradiation in fruits and seeds. The CDNA and proteins can be used to isolate homologies, for immunological screening and for positive
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Glycine max isoflavone O-methyltransferase clone srr1c.pk001.b16.
                                                                  Isoflavone O-methyltransferase; soybean; degradation; daidzein; Flavonoid; flower colour; growth; pollination; irradiation; ss.
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Isoflavone O-methyltransferase catalyses the first step in degradation of daidzein. Suppression of this enzyme will yield higher concentrations of this beneficial isoflavone in, e.g. soybean seed. Flavonoids serve as co-pigments in flower colour, stimulate pollen tube growth, attract pollenators, act as feeding deterrents and protect against UV irradiation in fruits and seeds. The CDNA and proteins can be used to isolate homologues, for immunological screening and for positive
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                                                                                                                                                               TTCTTGAACCAAATTGTCAAGGTGCATGGAACCAGTTGAAGAGGTGGGTTCATGAGGAAG 437
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Sequence 1053 BP; 323 A; 198 C; 226 G; 306 T; 0 other;
                                           Score 497.8; DB 21;
Pred. No. 6.5e-121;
0; Mismatches 317;
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Best Local Similarity 68.9%;
Matches 730; Conservative
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O-methyltransferase; soybean; degradation; daidzein; flower colour; growth; pollination; irradiation; ss.

Isoflavone (Flavonoid; 1 Glycine max

Glycine max isoflavone O-methyltransferase clone se4.pk0007.a11

(first entry)

26-SEP-2000

AAA29321

BP.

AAA29321 standard; cDNA; 1053

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                                                            TGAGTCTCTTCAATGAGGCTATGGCAAGTGATTCCCGAATGGTAGACTTGGCACTCAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GACAATCTCTCATCTCAAGCTAAACTGTGGAACTTCATTTATGGTTTTGCTGAATCACTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
preparation
                                                                                                                                                                          The present sequence encodes norcoclaurine 6-0-methyltransferase Also described is a method for the preparation of the secondary metabolite of a plant derived from coclaurine or reticuline.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
                                                                                                                                                                                                                                                                                                                                                                                  Score 209.2; DB 20; Length Pred. No. 6e-45; 0; Mismatches 463; Indels
useful for
                                                                                                                                                                                                                                                                                                                   Sequence 1041 BP; 320 A; 186 C; 245 G; 290 T; 0 other
   norcoclaurine 6-0-methyl-transferase
                                                                                                       5; Page 12; 27pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 53.6%;
Matches 558; Conservative
                                     secondary plant metabolite
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1014 TGGAAGCAGGGTTCCAAAGCTACAAAAATATCTCCCTTCACAGGATATTTGTCTCTTATTG 1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    980 AAAGIGCAGGATTTAGIGGTTGCAAAATCAGGCACATAGCGGCTATACAATCAGTCATTG 1039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATATGTTGGTGAACACTGGTGAAAGAGGGGACTAAAGAGGTTTTGGGAGAAATTGTGA 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trecraarateaaccaarregreeceacaretraarrecereceaccaaccaa 748
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                        GCCTCATGCGTTATCTAGCACACATGGATTCTTTGAGATAGTAAGAATCCATGACAACA 296
                                                      GGATATTACGATACTTGGTGAAATGGAAATACTGAGAGTGGAAAAATCTGATGATGGTC 271
                                                                                                                      AGAAGAAGTACGCGCTTGAACCTATTGCAACATTGCTTTCAAGGAATGCGAAGAGGGGTA 331
                                                                                                                                                                                      TGGTTCCAATGATTCTTGGAATGACTCAAAAGATTTTATGACTCCTTGGCATTCAATGA 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   riccacararcaagicaccererrigarerecereargrearriceaarrecerargaee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     834 ATTGTAAAGAAGCTATTTCAGGTGAAAGCAAACAGGAAAGTAGTTGTCATAGATACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   860 TGGCATTAGATGAGGAGTCAGACCATGAGCTTAGCAGCACACGATTGATCCTTGATATCG
                                                                                                                                                       TAGCTCCAATGGTTGAGTATTTTCTTGAACCAAATTGTCAAGGTGCATGGAACCAGTTGA
                                                                                                                                                                                                                                                     Aggangecniaagidacaanegic---anecninicagaaggccangegaangachahan
                                                                                                                                                                                                                                                                                       GGGACTITIATCAATAAAGACCCTGCATATAACAAGTCATTCAATGAGGCAATGGCTTGTG
                                                                                                                                                                                                                                                                                                                     degagractrogaagacaccroarcaaagccaarrarroargaaggcard
                                                                                                                                                                                                                                                                                                                                                     ATTCTCAGATGTTGAACTTGGCGTTTAGAGATTGCAATTGGG----TCTTTGAGGGACTGG
                                                                                                                                                                                                                                                                                                                                                                                    <u> AAACAAGGCTTCTCACTCTTCACTCTTTTCTCGGAAGTAGGATATGTTTTCAAGGTATTTC</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGAGGTGGGTTCATGAGGAAGATCTCACAGTATTTGAGGTCTCCTTAGGAACACCTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                     AATCCATTGTGGATGTTGGTGGAACTGGAATCACAGCAAAGATTATCTGTGAGGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human GDP-mannose 4,6-dehydratase (GM4,6D) DNA #13956
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                                                     944 ATGGATGTACACATGGCATGTATTATTAATGGAAAAGAGAAAAAAGAAGAAGATTGGAAG 1003
                                                                                                                                                   AAGCTCATCCATGCAGGGTACAAAGGGCATAAGATAACACAAAATTACTGCTGTACAA 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This cDNA encodes a polypeptide having the enzymatic activity of (S)-3, -hydroxy-N-methylcoclaurine 4'-0-methyltransferase (4'-OMT). A vector containing the DNA can be used to transform a microbe for the recombinant preparation of the enzyme. The enzyme can be used to prepare a secondary metabolite of a plant derived from reticuline which is useful as a raw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116
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                                                                                898 TIGGATTIGGACAIGAIGCICAACACIGGAGGAAAAGAGAGACIGAAGAGAAGAAGAAG 957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACTIGCCGAICTGGCAICTAAGCIICCTGTIICCGAIGTGAAIIGCGAIAATTIGIAIC 211
GTCGACATTGTCTTAAATGTGCAATCAGAACATCCTTA---TACCAAGATGAGACTGACT 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGGTCAAGCTCTCTTGTACAACATTTGCTTGGCTTCATAGATTCTAAGTGTCTAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGCTCAAGCTCATGTGGAAAATCATCTATGGTTTTGGAGATTCCCTAGTCCTCCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                               (S)-3'-hydroxy-N-methylcoclaurine 4'-O-methyltransferase; 4'-OMT; enzyme; secondary metabolite; reticuline; drug; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 178.4; DB 20; Length 1050;
Pred. No. 7.7e-37;
); Mismatches 481; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (S)-3'-hydroxy-N-methylcoclaurine 4'-O-methyltransferase encoding it
                                                                                                                                                                                                                                                                                                                                                                                                  (S)-3'-hydroxy-N-methylcoclaurine 4'-O-methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1050 BP; 313 A; 191 C; 252 G; 294 T; 0 other;
                                                                                                                                                                                      TCTCTTATTGAGATCTATCCTT 1085
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                                                                                                                                                                                                                                                                                                     standard; cDNA; 1050
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Similarity 51.3%;
28; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-DEC-1997;
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Local s.
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                                                                                                                                                                                                                                                                                                                                  AAX89255
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                                                                                                                                                                                                                                                                     RESULT 8
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246 ATCCCTCAAGC 256

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185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTAGAGAACTTGACAGGGACCAATAATTTGAGTTTTGTTGGTGGTGACATGTTCAACTCT 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fucosylation of glycoconjugates. These diseases include arthritis, transplant rejection, asthma, sepsis, reperfusion injury, stroke or infection. The GM4,6D peptide or a polynucleotide encoding it is also useful for manufacturing complex carbohydrates and as targets for screening small molecule antagonists of the activity of the enzyme. The polynucleotide is useful in developing an assay for defects in the enzyme, as well as in gene replacement therapy. Sequences ABX17942-ABX17944 and ABX17947-ABX33716 represent DNA molecules encoding Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
  cellular fucosylation; glycoconjugate fucosylation; transplant rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide, for manufacturing complex carbohydrates, or as targets for screening GM4,6D antagonists for treating e.g. arthritis, or transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              515 TTCAATGAGGCAATGGCTTGTGATTCTCAGATGTTGAACTTGGCGTTTAGAGATTGCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trcaardaggerargerargarrecegaaracragacrregeacreaaaarrecacr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     575 TGGGTCTTTGAGGGACTGGAATCCATTGTGGATGTTGGTGGTGGAACTGGAATCACAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             635 AAGATTATCTGTGAGGCTTTTCCTAAGCTGAAATGCATGGTGTTGGAACGTCCAAATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 AGAATTATCTGTGACGCATTTCCTAAGTTGAATGTGTTGTGTTGACCTTCGTCTTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                    arthritis; asthma; sepsis; reperfusion injury; stroke; infection; complex carbohydrate; gene replacement therapy; immunosuppressive; antiinflammatory; antiarthritic; antibacterial; cerebroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New composition comprising GDP-mannose 4,6-dehydratase (GM4,6D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 25; Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 13.6%; Score 158.2; DB 25; Length Best Local Similarity 76.9%; Pred. No. 9.5e-32; Matches 193; Conservative 0; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 256 BP; 61 A; 49 C; 65 G; 81 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 13958; 6pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     segdata.uspto.gov/seguence.html
                                                                                                                                                                                                                                                                                                                                97US-0984246.
98US-0149674.
99US-0333177.
                                                                                                                                                                                                                                                                     11-JUN-2001; 2001US-0878574
                                                                                                                                                                                                                                                                                                                                                                                                                        (GEMY ) GENETICS INST INC.
                                                                                           antiasthmatic; vasotropic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      755 ATCCCCAAGGC 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kriz R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-066673/06.
                                                                                                                                                                                US2002110548-A1
                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                22-NOV-1996;
                                                                                                                                                                                                                                                                                                                                   03-DEC-1997;
09-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sullivan F,
                                                                                                                                                                                                                            15-AUG-2002
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The invention relates to a composition comprising a human GDP-mannose 4,6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying GM4,6D inhibitors are useful for reducing inflammation in a mammalian subject and for treating or ameliorating diseases affected by the level of cellular fucosylation or diseases affected by the fucosylation of glycoconjugates. These diseases include arthritis, transplant rejection, asthma, sepsis, reperfusion injury, stroke or infection. The GM4,6D peptide or a polynucleotide encoding it is also useful for manufacturing complex carbohydrates and as targets for screening small molecule antagonists of the activity of the enzyme. The polynucleotide is useful in developing an assay for defects in the enzyme, as well as in gene replacement therapy. Sequences
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                                                                                                                                                                                             cellular fucosylation; glycoconjugate fucosylation; transplant rejection; arthritis; asthma; sepsitis; reperfusion injury; stroke; infection; complex carbohydrate; gene replacement therapy; immunosuppressive; antinflammatory; antiarthritic; antibacterial; cerebroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             enzyme, as well as in gene replacement therapy. Sequences
ABX17942-ABX17944 and ABX17947-ABX33716 represent DNA molecules encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New composition comprising GDP-mannose 4,6-dehydratase (GM4,6D) peptide, for manufacturing complex carbohydrates, or as targets for screening GM4,6D antagonists for treating e.g. arthritis, or transplant
                                                                                                                                                                            gene, ss; inflammation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72; Indels
                                                                                                                                           Human GDP-mannose 4,6-dehydratase (GM4,6D) DNA #5575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 266 BP; 91 A; 42 C; 60 G; 73 T; 0 other;
                                                                                                                                                                            Human; GDP-mannose 4,6-dehydratase; GM4,6D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 5577; 6pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human GM4,6D peptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           at segdata.uspto.gov/sequence.html
                                  ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kumar R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0984246.
98US-0149674.
99US-0333177.
                                  ABX23518 standard; cDNA; 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                        96US-0753233
                                                                                                                                                                                                                                                                                                                                                                                                                    11-JUN-2001; 2001US-0878574
                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                          antiasthmatic; vasotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kriz R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sullivan F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-NOV-1996;
                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JUN-1999;
                                                                                                       10-FEB-2003
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                                                                       ABX23518;
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Matches
RESULT 10
                  ABX23518
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140

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Gaps

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84

144 200 198

RESULT 11 ABX19667 260

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259 ATGGAATCTTTGAGATCCATGAGAGCCAAGAAGATCATGAACTAACATATGCTCTAACCC 318
  enzyme, as well as in gene replacement therapy. Sequences SARI/1944 and ABXI/1947-ABXI/3943/16 represent DNA molecules encoding human GM4.6D peptides of the invention.

Note: The sequence data for this patent did not form part of the printed
                                                                   Note: The sequence data for this patent did not form part of the printer specification but was obtained in electronic format directly from USPTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 ACATAAT----ACAGAACCATGCCAAACCCATTTCTCTTTCTGACTTGGTCTCTACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        199 rrcaaarrccaccagcraacgcracrrrrcrecagcgcrrcarecerrcrreecacaca
                                                                                                                                                                                                                                                                                                                                                                                   85 AGCTATATGGGCACCTAAGACCTATGTGTCTTAAGTGGGCCTGTTCAACTAGGTATTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 ACATAATCCACAGCCATAGCCATGGCCAACCCATTACTTTTCAGAGTTGGTGTCAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TACAAGTCCCACCAACTAAAACTCGTCAGGTGCAGAGCCTCATGCGTTATCTAGCACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGGATTCTTTGAGATAGTAAGAATCCATGACAAAAAA---AGCATATGCTCTCACTG
                                                                                                                                                                                                                                                                                             21 CATTAAACAATGGCCGTAAAGCAAGTGAGATTTTTCAAGGTCAAGCTCTTGTACAAAC
                                                                                                                                                                                                                                                                                                                                       25 cricaargaaraaccaaaaagaaarrgagcrerrrgaggggggaarcrergracargc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maize; corn; caffeic O-methyltransferase; lignin; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             318 CTGCTTCAGAGTTACTTGTCAAAAGCAGTGAGCTTAGTTTAGCTCCAATGGTT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        crecarcaaserrereararararararararrererarererere
                                                                                                                                                                                                    Score 142.2; DB 25; Length 381; Pred. No. 1.8e-27;
                                                                                                                                                                                                                                              0; Mismatches 108; Indels
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                                                                                                                                                          Seguence 381 BP; 109 A; 88 C; 69 G; 115 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           caffeic O-methyltransferase cDNA.
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139..1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang X;
                                                                                                                at seqdata.uspto.gov/sequence.html.
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                                                                                                                                                                                                    12.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                   236; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-204667/17.
P-PSDB; AAY05661.
                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX25200 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9910498-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bowen BA,
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                                                                                                                                                                                                                           940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; GDP-mannose 4,6-dehydratase; GM4,6D; gene; ss; inflammation; cellular fucosylation; glycoconjugate fucosylation; transplant rejection; arthritis; asthma; sepsils; reperfusion injury; stroke; infection; complex carbohydrate; gene replacement therapy; immunosuppressive; antiinflammatory; antiarthritic; antibacterial; cerebroprotective;
                                                 820
                                                                                                                                  880
                                                                                                                                                                               181
                                                                                                                                                                                                                                                                     241
                                                                                    CAAGCIGAIGCAGIGCIACIAAAGIGGGIITITACAIAATIGGACCGACGAAAAIIGCAIA 121
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AACTIGACAGGGACCAATAATITGAGTTTTGTTGGTGGTGACATGTTCAACTCTATCCCT
                                              761 AAGGCTGATGCAGTTCTGCTTAAGTTGGTTTTACATAATTGGAATGACAACGATTGCATG
                                                                                                                                     AAGATATTAGAAAATTGTAAAGAAGCTATTTCAGGTGAAAGCAAAACAGGAAAAGTAGTT
                                                                                                                                                                             AAGATCCTGCAAAAGTGTAGAGATTCTATTTCAAGCAAAGGCAACAGTGGAAAAGTGATT
                                                                                                                                                                                                                           GTCATAGATACTGTGATAAACGAAACAAAGATGAGCGCCCAAGTTACTGAACTAAAGCTC
                                                                                                                                                                                                                                                                   <u> arcanaganeccenanaganeganecnaganegeceegananegeneganaganegenn</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human GDP-mannose 4,6-dehydratase (GM4,6D) DNA #1724.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP
                                                                                                                                                                                                                                                                                                                CTTATGGATGTACACATG 958
                                                                                                                                                                                                                                                                                                                                                          242 AGTITGGACATIATIATG 259
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97US-0984246.
98US-0149674.
99US-0333177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABX19667 standard; cDNA; 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kumar
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09-SEP-1998;
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This DNA sequence encodes a caffeic O-methyltransferase (see AAYO5661)

of maize. A polynucleotide having this sequence can be amplified from a cDNA library prepared from premeiotic to unfuncleate tassel from maize A632 using the primer pair given in AAX2525 and AAX25226. The invention provides methods and compositions relating to altering lighin biosynthesis and/or the lighin composition of plants. Isolated nucleic acids (see AAX25196-156) that code for proteins (see AAY05657-77) involved in lighin biosynthesis are claimed. Also claimed are recombinant expression cassettes, host colls (especially maize or sorghum), and transgenic plants and cells (especially maize or sorghum), and transgenic plants and colls (aspecially maize or sorghum), and transgenic plants and colls in plant plant coll with a recombinant expression cassette comprising a lighin biosynthesis. A claimed method involves transforming a plant cell with a recombinant expression cassette comprising a lighin biosynthesis polynucleotide for a time sufficient to modulate (preferably increase) lignin biosynthesis in the plant. The plant lignins can be used as chemical feedstock. Plant material of increased lignin content can be used as a fuel source, and in the pulp and page; industry. Decreased lignin content and in the pulp and page; industry.
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                           Nucleic acids encoding plant lignin biosynthesis enzymes – used to
transform plants to modulate lignin biosynthesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.4%; Score 120.2; DB 20; Length Best Local Similarity 54.0%; Pred. No. 1.8e-21; Matches 292; Conservative 0; Mismatches 243; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1412 BP; 324 A; 400 C; 375 G; 313 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and in the pulp and paper industry. Decrea improves the digestibility of fodder crops.
                                                                                                            Claim 2; Page 119-121; 166pp; English.
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The invention relates to methods for producing forage legumes or woody plants having altered lignin composition. Methods for transforming forage legumes with a DNA construct comprises alfalfa caffein acid 3-0. methyltransferase (CCOMT) and the construct comprises alfalfa caffein acid 3-0. methyltransferase (CCOMT) and the corresponding promoter, resulting in the down regulation of the corresponding proposesion. The methods are useful for down-regulation of the curresponding homologous OMT genes, gene silencing, reduced OMT activity corresponding homologous OMT genes, gene silencing, reduced OMT activity levels, reduced lignin content, and modified lignin composition in transgenic plants, and increased digestibility of transgenic plant materials in ruminant animals. The expression of CCOMT transgene produces the angle lignin to guaiacyl lignin ratio in the transformed plant and greatly improved forage in vivo digestibility, and for making lignins with altered dimer bonding patterns. Transforming forage legumes in the transformed plants having modified lignin content and commonities to the content and commonities of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of
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                                                                                                                                                                                                                                                                                 Alfalfa, caffeoyl CoA 3-0-methyltransferase, CCOMT, lignin, woody plant, forage legume, transgenic plant, paper industry, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     improve pulping characteristics for the paper industry. The present cDNA sequence encodes alfalfa caffeoyl CoA 3-0-methyltransferase (CCOMT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transforming forage legumes for modifying lignin composition and increasing in vivo digestibility comprises transforming plants with lignin biosynthetic enzyme genes under lignification-associated tissue specific promoter -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a /*tag= a /*tag= /product= "Alfalfa caffeoy1 CoA 3-O-methyltransferase
                                                                                                                                                                                                                         Medicago sativa caffeoyl CoA 3-0-methyltransferase (CCOMT) cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1..1098
                                                       AAD19546 standard; cDNA; 1098 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CCOMT) protein"
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Best Local Similarity 52.7%;
Matches 309; Conservative
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RESULT 13
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7

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Dixon RA, Ni W;
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                  13-OCT-1994.
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                                                                                                                                                                                                                                                                                          CGATTGTCTCAAAATATCCCCACTATAAAGGGTATAAATTTTGATTTACCCCATGTCATTG
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                                                                                                                                                                                                                                                                                                                                                                         AAGATGCTCCATCTTATCCAGGAGTTGAGCATGTTGGTGGAGACATGTTTGTCAGTATTC
                                                                                                                                                                                                                                                                                                                                                                                                                 CCAAGGCTGATGCAGTTCTGCTTAAGTTGGTTTTACATAATTGGAATGACAACGATTGCA
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/note= "the inverted complement of this portion
of the COMT gene was the antisense fragment
used to reduce tobacco lignin content"
541..1016
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of the COMT gene was the antisense fragment
used to reduce alfalfa lignin content"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGITIGAGGAICTIGCCAAAGGIGCTGGAITCCAAGGITICAAAGT 1046
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55..1152
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10..541
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>AAAATTTGTCAGGAAGCAACAATTTGACATTTGTTGGTGGGGACATGTTTAAATGCATCC</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 764 AAGATGCTCCATCTTATCCAGGAGTTGAGCATGTTGGTGGAGACATGTTTGTCAGTATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAAGGCTGATGCAGTTCTGCTTAAGTTGGTTTTACATAATTGGAATGACAATGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         524 CTTATGGAATGACAGCCTTTGAATACCATGGAACAGATCCAAGGTTTAACAAGGTTTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              519 ATGAGGCAATGGCTTGTGATTCTCAGATGTTGAACTTGGCGTTTAGAGATTGCAATTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               584 ACAAGGGGAIGTCIGAICACTCIACCAICACAAIGAAGAAAAITCIIGAGACCIACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         644 GTTTTGAAGGCCTTAAATCTCTTGTTGATGTAGGTGGTGGTACTGGAGCTGTAATTAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          639 TTAICTGIGAGGCTTTTCCTAAGCTGAAAIGCAIGGIGTIGGAACGTCCAAAIGTIGIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAAAGGCTGATGCTGTTTTTATGAAGTGGATTTGTCATGACTGGAGTGATGAGGCACTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGAAGATATTAGAAAATTGTAAAGAAGCTATTTCAGGTGAAAGCAAAACAGGAAAAGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGICATAGATACTGTGATAACGAAAACAAAGATGAGCGCCAAGTTACTGAACTAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         935 TTGTGGCAGAATGCATACTTCCAGTGGCTCCAGATTCAAGCCTGGCCACAAAAGGTGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCTTAGGAACACCTTTCTGGGACTTTATCAATAAAGACCCTGCATATAACAAGTCATTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    579 TCTTTGAGGGACTGGAATCCATTGTGGATGTTGGTGGTGGAACTGGAATCACACAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alfalfa COMT clone pCOMT1, obtained from a cDNA library in lambda ZAP II, was the basis of antisense genes used to reduce the lignin content of E.g. tobacco and alfalfa.

(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1341;
                                                                                                                                                                                                                                                                                                                                                                             Reducing lignin content in plants - by transfection with an anti-sense gene for caffeic acid 3-0-methyl-transferase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    996 ATTGGAAGAACTCTTCATGGAAGCAGGGTTCCAAAAGCTACAAAAT 1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 118; DB 15; Length 13
Pred. No. 6.6e-21;
0; Mismatches 265; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1055 AGTTTGAGGATCTTGCCAAAGGTGCTGGATTCCAAGGTTTCAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1341 BP; 402 A; 252 C; 280 G; 407 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                884 richantringangancricorargaggeorogge
                                                                                                                                     (ROBE-) ROBERTS NOBLE FOUND INC SAMMUEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 21-23; 39pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 10.2%;
Local Similarity 52.7%;
des 309; Conservative
94WO-US03356
                                                                    93US-0045263
                                                                                                                                                                                                                                                                    WPI; 1994-333204/41.
P-PSDB; AAR63203.
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RESULT 15

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990S-0139460.
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990S-0146386-

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990S-0147038-

990S-0147024-

990S-01471204-

990S-0147120-

990S-01471303-

990S-0147416-

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990S-0148171-

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99US-0149723.
99US-0149929.
                                                                                                                                                                                                                                                                                                                                                                                           02-AUG-1999;
02-AUG-1999;
02-AUG-1999;
03-AUG-1999;
04-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-AUG-1999;
10-AUG-1999;
11-AUG-1999;
12-AUG-1999;
13-AUG-1999;
14-AUG-1999;
18 - 70x - 1999;

18 - 70x - 1999;

18 - 70x - 1999;

18 - 70x - 1999;

18 - 70x - 1999;

21 - 70x - 1999;

23 - 70x - 1999;

24 - 70x - 1999;

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22 - 70x - 1999;

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24 - 70x - 1999;

25 - 70x - 1999;

26 - 70x - 1999;

27 - 70x - 1999;
                                                                                                                                                                13-JUL-1999;
14-JUL-1999;
15-JUL-1999;
16-JUL-1999;
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19-JUL-1999;
19-JUL-1999;
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20-AUG-1999;
20-AUG-1999;
                                                                                                                                                                                                                      19-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                     28-JUL-1999;
  Hybridisation assay, genetic mapping, gene expression control, protein identification, signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                       Arabidopsis thaliana DNA fragment SEQ ID NO: 29270.
        AAC40707 standard; DNA; 1267 BP
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990S-0123180.
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990S-0136329.
990S-0136329.
                                                                                                                                                 25-FEB-2000; 2000EP-0301439
                                       17-OCT-2000 (first entry)
                                                                                                    Arabidopsis thaliana
                                                                                                                   EP1033405-A2
                                                                                                                                                                                                                    06-APR-1999,
16-APR-1999,
19-APR-1999,
19-APR-1999,
23-APR-1999,
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30-APR-1999,
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05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
11-MAY-1999;
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25-MAY-1999;
27-MAY-1999;
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                                                                                                                                  06-SEP-2000,
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1-JUN-1999
                        AAC40707;
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937

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99US - 0149902,
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Best Local Similarity 54.9
Matches 225; Conservative
                                                               26-AUG-1999;
27-AUG-1999;
27-AUG-1999;
27-AUG-1999;
30-AUG-1999;
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16-SEP-1999;
16-SEP-1999;
16-SEP-1999;
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TIGCAAITGGGTCTTTGAGGGACTGGAATCCAITGTGGATGTTGGTGGTGGACTGGAACTGGAAT 627
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ORGANISM: Glycine
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        GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-09-500-569-3
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Sequence 17, Appl
Sequence 3, Appli
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Sequence 165, Ap
Sequence 974, Appli
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US-09-500-569-17

Sequence 17, Application US/09500569

Patent No. 6329204

GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Refalski, Antoni
APPLICANT: Shen, Jennie
TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase Homologs
FILE REPERENCE: BB1327 US NA
CURRENT APPLICATION NUMBER: US/09/500,569

CURRENT APPLICATION NUMBER: US/09/500,569

CURRENT FILING DATE: 1999-February-10

SARLIER FILING DATE: 1999-February-10

SOFTWARE: Microsoft Office 97

SEQUENCE: AND OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE O
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54.5%;
Best Local Similarity 5... Matches 228; Conservative
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,288
FILING DATE: 10-MAR.1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9119279.9
FILING DATE: 10-SEP-1991
PRIOR APPLICATION NUMBER: PCT/GB92/01460
FILING DATE: 09-SEP-1991
APPLICATION NUMBER: PCT/GB92/01460
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: KOKULIS, Paul N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 206860/SEB36543/UST
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Patent No. 5959178
                                                                                                                                                                                                                                                                                                                                                                                                                     VAN DOORSSELAERE, Ja
FRITIG, Bernard J.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KNIGHT, Mary E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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JOUANIN, Lise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: MO
TITLE OF INVENTION: PL
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
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RY: U.S.A.
20005-3518
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APPLICANT: VAN DO
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US-08-204-288-1
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988 AGAAGAAGAITGGAAGAAACTCTTCATGGAAGCAGGGTTCCAAAGCTACAAAATATCTCC 1047
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                                                                                                                                            448 ATTTGAGGTCTCCTTAGGAACACCTTTCTGGGACTTTTATCAATAAAGACCCTGCATATAA
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       Length 1368;
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APPLICANT: Chiang, Vincent L
APPLICANT: Teal, Chung-Jui
APPLICANT: Podila, Gopi
TITLE OF INVENTION: Genetic Engineering of Wood Color
TITLE OF INVENTION: in Plants
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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Score 109.8; DB 2;
Pred. No. 1.1e-20;
0; Mismatches 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1048 CTTCACAGGATATTTGTCTCTTATTGAGATC 1078
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53202
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Milwaukee
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988 AGAAGAAGATTGGAAGAAACTCTTCATGGAAGCAGGGTTCCAAAAGGTACAAAATATCTCC 1047
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US-09-463-323-1

Sequence 1, Application US/09453323

Patent No. 6441272

GENERAL INFORMATION:

APPLICANT: Ye, Zheng-Hua

TITLE OF INVENTION: MODIFICATION OF LIGNIN CONTENT AND COMPOSITION IN

TITLE OF INVENTION: PLANTS

FILE REPERENCE: 235.0090101

CURRENT APPLICATION NUMBER: US/09/453,323

CURRENT FILING DATE: 1999-12-02

PRIOR FILING DATE: 1998-12-02

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin Ver. 2.0
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9.4%; Score 109; DB 4; L
Best Local Similarity 53.1%; Pred. No. 2e-20;
Matches 232; Conservative 0; Mismatches 205;
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US-08-204-288-3
; Sequence 3, Application US/08204288
; Patent No. 5959178
; GENERAL INFORMATION:
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LENGTH: 1507
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DEVELDOPRENTAL STAGE: Gour year old sapling
DEVELOPMENTAL STAGE: undergoing lignification in summer
TISSUE TYPE: secondary xylem
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Pred, No. 1.2e-20;
0; Mismatches 312;
                                                                                                                                                                                                                                                                                                                                                                                                NAME: Gemignani, Joseph A
REGISTRATION WUMBER: 19,482
REPERENCE/DOCKET NUMBER: 66040/9627
TELECOMMUNICATION INFORMATION:
TELECAX: (414) 277-656
TELEX: 262057
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1503 base pairs
TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: linear
                                               APPLICATION NUMBER: US/08/715,325
                                                                                         FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US60/007727
FILING DATE: 30 NOV 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA to total mRNA
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Best Local Similarity 49.6%;
Matches 313; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: cDNA to mRNA HYPOTHETICAL: no
CURRENT APPLICATION DATA:
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583 GATCCAAGGTTTAACAAGGTTTTCAACAAGGGAATGGCTGATCACTCTACCATCACAATG 642
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                                                                                                                                                                                                                                                                                                                   824 ATATTAGAAAATTGTAAAGAAGCTATTTCAGGTGAAAGCAAAACAGGAAAAGTAGTTGTC 883
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704 TIGICAGGAAGCAACAATITGACATTTGTTGGTGGGGACATGTTTAAATGCATCCCCAAG 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        674 GTGTTGGAACGTCCAAAIGTTGTGGAAAATTTGTCAGGAAGCAACAATTTGACATTTGTT 733
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                                                                             565 GCTCCAGCTTACCCTGCTGTCGAGCACGTTGGTGGCGACATGTTTGCCAGTGTGCCAAAA
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APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
APPLICANT: Shen, Jennie
TITLE CANTESHER SHEN, Jennie
TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase Homologs
FILE REFERENCE: BB1327 US NA
FULER PELING APPLICATION NUMBER: US/09/500, S69
CURRENT FILING DATE: 2000-02-09
EARLIER PILING DATE: 1999-February-10
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1370;
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Pred. No. 4.1e-20;
0; Mismatches 292;
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Patent No. 6329204
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.3%;
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Best Local Similarity 50.9
Matches 315, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           884 ATAGATACTGTG
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US-09-500-569-3
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                                                                                                                                                                                                                                                                      MODIFICATION OF LIGNIN SYNTHESIS IN PLANTS
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,288
FILING DATE: 10-MAR-1994
CLASSIFICATION: 800
PRIOR APPLICATION NUMBER: GB 9119279.9
FILING DATE: 10-SEP-1991
PRIOR APPLICATION NUMBER: CFT/GB92/01460
FILING DATE: 09-SEP-1991
APPLICATION NUMBER: D9-SEP-1992
ATTORNEY/AGENT INPORMATION:
NAME: REGISTRATION NUMBER: 16,773
REGISTRATION NUMBER: 16,773
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REGISTRATION NUMBER: 16,773
REGISTRATION STATESTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
STREET: 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: D. C.
COUNTRY: U.S.A.
ZIP: 20005-3518
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                 INZE, Dirk G.
JOUANIN, Lise
KNICHT, Mary E.
VAN MONTAGU, Marc
LEGRAND, Michel
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington
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Les 259; Conserv
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APPLICANT:
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459 CCTTAGGAACACCTTTCTGGGACTTTATCAATAAAGACCCTGCATATAACAAGTCATTCA 518
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                                                                                                                                                                                                                                                       648 GATTTGAAGGCCTAAATTCCATTGTTGATGTTGGTGGAACGGGTGCTACTGTTAACA 707
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                                                                                                                                                                                                                                                                                                                                                                                                      699 AAAAITTGTCAGGAAGCAACTATTGACATTTGTTGGTGGGGACATGTTTAAATGCATCC 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                      768 GAGATGCTCCAACTTACCCCGGTGTCGAGCACGTTGGTGGCGACATGTTTGCTAGTGT-G 826
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                                                        528 CCTATGGAATGCAAGCATTTGAGTACCATGGCACAGATCCAAGATTCAACAAAGTGTTCA
                                                                                                        519 ATGAGGCAATGGCTTGTGATTCTCAGATGTTGAACTTGGCGTTTAGAGATTGCAATTGGG
                                                                                                                                                                                                      579 TCTTTGAGGGACTGGAATCCATTGTGGATGTTGGTGGAACTGGAATCACAGCAAAGA
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APPLICANT: Cahoon, Rebecca E.
APPLICANT: Stalashi, Antoni
APPLICANT: Shealshi, Antoni
APPLICANT: Sheal, Jennie
TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase Homologs
FILE REPERENCE: BB1327 US NA
CURRENT APPLICATION NUMBER: US/09/500,569
CURRENT FILING DATE: 2000-02-09
EARLIER APPLICATION NUMBER: 60/119,587
EARLIER PILING DATE: 1999-Pebruary-10
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
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Pred. No. 9.7e-17;
0; Mismatches 191; Indels
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Patent No. 6329204
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Best Local Similarity 52.4'
Matches 210; Conservative
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                                                                                                                                                 971 AATGGAAAAGAGAAAAAGAAGAAGATTGGAAGAAACTCTTCATGGAAGCAGGGTTCCAA 1030
                                                                                                                                                                                                 1054 CGTGGGAAAGAGAGACAGAGAAAGAGTTTGAGGCTCTGGCCAAAGGGTCTGGATTCCAA 1113
                                                                                                994 retadetregecacaaaaggrergericacaregargrearearerrgecacaraaree 1053
943 G-----ACAATGGGAAGGTGATTGTGGCAGAATGCATTCTTCCAGTGGCTCCAGAC 993
                                                     914 GAGCGCCAAGTTACTGAACTAAAGCTCCTTATGGATGTACACA---TGGCATGTATTATT 970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: INZE, ...
APPLICANT: OCUANIN, Lise
APPLICANT: KNIGHT, Mary E.
APPLICANT: VAN MONTAGU, Marc
APPLICANT: LERAND, Machel
THE OF INVENTION: PLANTS
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52.9%; Pred. No. 3.8e-17;
tive 0; Mismatches 205; Indels
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COUNTRY: U.S.A.
ZIP: 2005-3518
COMPUTER REAGABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,288
FILING DATE: 10-MAR-1994
CLASSIFICATION NUMBER: B09
PRIOR APPLICATION NUMBER: B09
PRIOR APPLICATION NUMBER: PCT/GB92/01460
FILING DATE: 10-SEP-1991
PRIOR APPLICATION NUMBER: PCT/GB92/01460
FILING DATE: 09-SEP-1991
PRIOR APPLICATION NUMBER: PCT/GB92/01460
FILING DATE: 09-SEP-1992
ATPLING DATE: 09-SEP-1992
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REPERENCE/DOCKET NUMBER: 206860/SE55543/UST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                             1114 GGTTTCCGAGTTGTTTGCT 1132
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APPLICANT: VAN DOORSELAERE, Jan
APPLICANT: FRITIG, Bernard J.M.
APPLICANT: INZE, Dirk G.
APPLICANT: JOUANIN, Lise
                                                                                                                                                                                                                                                  1031 AGCTACAAAATATCTCCCT 1049
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08204288 Patent No. 5959178
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Matches 231; Conservative
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STRANDEDNESS: sing
TOPOLOGY: linear
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US-08-204-288-4
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            907 TITITGAAGAAATGITATGAAGCACTICCA-----ACCAAIGGGAAGGIGAICCIT 957
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                                                                                  884 ATAGATACTGTGATAAACGAAAACAAAGATGAGCGCCAAGTTACTGAACTAAAGCTCCTT
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Pred. No. 6.3e-16;
0; Mismatches 259;
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Lignin
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TITLE OF INVENTION: Materials and Methods for
TITLE OF INVENTION: Modification of Plant Lig
FILE SEPERBENCE: 11000.1003c4U
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT APPLICATION NUMBER: US 08/975,316
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR PILING DATE: 1997-11-21
PRIOR PILING DATE: 1997-01-21
PRIOR PILING DATE: 1996-09-11
PRIOR PILING DATE: 1996-09-11
PRIOR FILING DATE: 1996-09-11
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 405
NUMBER OF SEQ ID NOS: 405
SEQ ID NO 107
TOWN THE PRESERVE OF WINGOWS Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 107, Application US/09615192A
Patent No. 6410718
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US-09-615-192A-107
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Matches 280; Conservative
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                                                  704 ITGTCAGGAAGCAACAATTTGACATTTGTTGGTGGGGACATGTTTAAATGCATCCCCAAG 763
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                                                                                              GCCICTACCTATCCTGGTGTGAGCATGTGGGAGAGATATGTTTGAAAGTGTGCACAA
                                                                                                                                              GCTGATGCAGTTCTGCTTAAGTTGGTTTTACATAATTGGAATGACAACGATTGCATGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Chiang, Vincent L
APPLICANT: Chiang, Vincent L
APPLICANT: Carraway, Daniel T
APPLICANT: Garraway, Daniel T
APPLICANT: Smeltzer, Richard H
TITLE OF INVENTION: Production of Syringyl Lignin in Gymnosperms
FILE REFERENCE: 50617
CURRENT FILING DATE: 1997-12-16
EARLIER APPLICATION NUMBER: US 60/033,381
EARLIER APPLICATION NUMBER: US 60/033,381
NUMBER OF SEQ ID MOSE: 1996-12-16
NUMBER OF SEQ ID NOS: 1096-12-16
SOFTWARE: Patentin Ver. 2.0
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Pred. No. 1.7e-16; 0; Mismatches 309;
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/08991677A Patent No. 6252135 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Liquidambar styraciflua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.2%;
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Best Local Similarity 50.1
Matches 325, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | NAME/KEY: CDS
| LOCATION: (67)..(1170)
| US-08-991-677-5
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APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka
APPLICANT: and GRIERSON, Alastair W.
TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
NUMBER OF SEQUENCES: 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score.86.2; DB 4; Length 6 Pred. No. 2.6e-14; O; Mismatches 173; Indels
Modification of Plant Lignin Content
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COMPUTER READABLE FORM:
MEDLUM TYPE: Diskette
COMPUTER: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
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2601 Elliott Avenue, Suite 4185
                CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT PILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR PILING DATE: 1997-11.21
PRIOR PAPLICATION NUMBER: US 08/975,316
PRIOR PILING DATE: 1996-09-11
PRIOR PILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR PILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 4005
SOFTWARE: PastSEQ for Windows Version 3:0
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Patent No. 5952486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

Best Local Similarity 52.3%;
Matches 190; Conservative (
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ADDRESSEE: Law Office
STREET: 2601 Elliott
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Pinus radiata
  TITLE OF INVENTION:
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                                                                        987 ACGAGCCTAGCGACCAAGAATGTGATCCACATCGACTGCATCATGTTGGCCCACAACCCA 1046
                                                                                                                             971 AATGGAAAAGAGAGAAAAAAAAATTGGAAGAAACTCTTCATGGAAGCAGGGTTCCAA 1030
                                                                                                                                                                               1047 GGCGGGAAAGAGAGGACACAGAAGGAGTTCGAGGCATTGGCCAAAGGGGCCGGATTTCAG 1106
                         914 GAGCGCCAAGTTACTGAACTAAAGCTCCTTATGGATGTACACA---TGGCCATGTATTATT 970
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Pred. No. 2.5e-15;
0; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Blokeberg, Leonard N. APPLICANT: Blokeberg, Leonard N. APPLICANT: Havukkala, 11kka
APPLICANT: Havukkala, 11kka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 11000,1003c4U
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1995-09-11
PRIOR FILING DATE: 1996-09-11
PRIOR FILING DATE: 1996-09-11
PRIOR FILING DATE: 1996-09-11
PRIOR FILING DATE: 1996-10-09
NUMBER OF SEQ ID NOS: 405
NUMBER OF SEQ ID NOS: 405
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                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 174, Application US/09615192A
Patent No. 6410718
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                                                                                                                                                                                                                                  1031 AGCTACAAAAT 1041
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Best Local Similarity 58.8
Matches 174; Conservative
                                                                                                                                                                                                                                                                                          1107 GGCTTCCAAGT 1117
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                                                                                                                                                                                                                                                                                                                                                                                              -09-615-192A-174
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LENGTH: 381
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                                                                                                                                                                                                                                                                                                                                Length 744;
                                                                                                                                                                                                                                                                                                                         Score 86.2; DB 4; Length 7
Pred. No. 2.7e-14;
0; Mismatches 173; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 10-MAR-1994
CLASSIFICATION: 800
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                                             NUMBER OF SEQ ID NOS: 405
SOFTWARE: FastSEQ for Windows Version 3.0
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GENERAL INFORMATION:
APPLICANT: VAN DOORSELAERE, Jan
APPLICANT: FRITG, BETRAR J.M.
APPLICANT: INZE, Dirk G.
APPLICANT: JOUANIN, Lise
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Patent No. 5959178
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ZID: 20005-3518
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

"MEDIUM TYPE: Floppy disk

"MEDIUM TYPE: ISM PC COMPALIBLE
"MANTHER: ISM PC COMPALIBLE
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VAN MONTAGU, Marc
                                                                                                                                                                                                                                                                                                                            7.4%;
                 PRIOR FILING DATE: 1998-10-09
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Best Local Similarity 52.3
Matches 190; Conservative
                                                                                                                                                                                    TYPE: DNA
ORGANISM: Pinus radiata
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TITLE OF INVENTION: PI
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                  SEQ ID NO 51
LENGTH: 744
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US-08-204-288-6
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Patent No. 6410718
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Bavukkala, Ilka
ITLE OF INVENTION: Materials and Methods for the
FITLE OF INVENTION: Modification of Plant Lignin Content
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,000
FILING DATE: September 11, 1996
ATTORNEY/AGENT IRPORMATION:
NAME: SLEATH, Janet
REGISTRATION NUMBER: 37,007
REGISTRATION INDRER: 37,007
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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3ER: US 08/975,316
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PRIOR FILING DATE: 1997-11-21
PRIOR PELICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
                                  APPLICATION NUMBER: US/08/975,316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH- 744 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 206-269-0563
TELEX:
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                                                                     FILING DATE:
CLASSIFICATION:
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US-09-615-192A-51
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US-08-975-316-51
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947 GCTCTACCAGACAATGGAAAGGTGATTGTTGATGACCATTTTACCAGTGAAACCAGAC 1006
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7.1%; Score 82.6; DB 2; Length 1471;
Best Local Similarity 46.2%; Pred. No. 3.4e-13;
Matches 314; Conservative 0; Mismatches 359; Indels 6.
PRIOR APPLICATION DATA,

APPLICATION NUMBER: GB 9119279.9

FILING DATE: 10-SEP-1991

PRIOR APPLICATION NUMBER: CCT/GB92/01460

FILING DATE: 09-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: CONCULTS, Paul N.

REGISTRATION NUMBER: 16,773

REFERENCE/COCKET NUMBER: 206860/SEB36543/UST

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFANE: (202) 861-3000

TELEFAX: 6714627 CUSH

INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:

LENGTH: 1471 base pairs

TYPE: nucleic acid STRANDENCES:

LENGTH: 1471 base pairs

TYPE: nucleic acid STRANDENCES: single

TOPOLOGY: linear

TOPOLOGY: linear

TOPOLOGY: linear

TOPOLOGY: linear
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Search completed: November 10, 2003, 01:53:12 Job time : 105 secs
1181 TAGATTTCTACTGTACATT 1199
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(without alignments)
8029.308 Million cell updates/sec
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11. (cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

12. (cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

13. (cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

14. (cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

15. (cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

16. (cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

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13. (cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

14. (cgn2_6/ptodata/2/pubpna/US10M_PUB.seq:*

15. (cgn2_6/ptodata/2/pubpna/US10M_PUB.seq:*

16. (cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2141354 segs, 1595478879 residues
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                       Copyright
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 13958, A Sequence 1726, Ap Sequence 1726, Ap Sequence 23, Appl Sequence 24, Appl Sequence 5, Appl Sequence 10987, A Sequence 13, Appl Sequence 12, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 5, Appl Sequence 5, Appl Sequence 5, Appl Sequence 5, Appl Sequence 107, Appl Sequence 107, Appl Sequence 107, Appl Description 0.05-09-878-574-13958 0.05-09-878-574-1726 0.05-09-878-574-1726 0.05-09-878-574-3502 0.05-09-878-574-3502 0.05-09-878-574-3502 0.05-09-878-574-10987 0.05-09-129-298-3 0.05-09-129-298-3 0.05-09-129-298-3 0.05-09-878-574-13211 0.05-09-129-298-3 0.05-09-878-574-13211 0.05-09-978-974-32512 0.05-09-978-974-3282 0.05-09-978-974-3282 0.05-09-978-974-3282 0.05-09-978-978-3582 0.05-09-978-978-3582 0.05-09-978-978-3582 0.05-09-978-978-3582 0.05-09-978-978-3582 Query Match Length DB 1111 1101 1009 1009 1009 106.8 100.2 94.6 92.6 158.2 142.8 142.2 120.2 107.4 Result

Sequence 174, App Sequence 127, App Sequence 51, Appl	രംത്ത	6 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	227 227 227 227	Sequence 28 Sequence 28 Sequence 22 Sequence 22 Sequence 19 Sequence 19	Sequence 1047, Ap Sequence 150, App Sequence 41, Appl Sequence 893, App Sequence 149, App Sequence 16, Appl
693-17 693-12 693-51		US-09-878-574-97 US-10-289-757-43 US-09-923-876-518 US-09-878-574-48	US-10-174-693-18 US-10-213-473-25 US-10-174-693-18 US-10-174-693-19 US-10-213-473-27	4 US-10-213-4/3-2 4 US-10-213-473-2 5 US-10-213-473-2 5 US-10-289-757-4 5 US-10-213-473-2	12 US-09-923-8/5-104/ 12 US-10-289-757-150 12 US-10-289-757-41 9 US-09-923-876-893 12 US-10-289-757-149 12 US-10-289-757-40
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ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: Byrum, Joseph R.
APPLICANT: Byrum, Joseph R.
APPLICANT: Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Plants
FILE OF INVENTION: Plants
FILE REPERRICE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
FILE REPERRICE: 2001-12-21
PRIOR PILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
SEQ ID NO. 13958
LENGTH: 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701068136H1
US-09-878-574-13958
US-09-878-574-13958
; Sequence 13958, Application US/09878574
; Patent No. US20020110548A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 193; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                  Length 381;
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Pred. No. 5.4e-22;
0; Mismatches 243; Indels
                                                                                                                                                                                                                                                               DB 10;
                                                                                                                                                                                                                                                           Score 142.2; DB 10;
Pred. No. 2.6e-28;
0; Mismatches 108;
                                              LENGTH: 381
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: LIB3028-034-Q1-B1-D6
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ITILE OF INVENTION: Genes Encoding Enzymes for TITLE OF INVENTION: Biosynthesis and Uses The CURRENT APPLICANTON NUMBER: US/10/361,460
CURRENT APPLICANTON NUMBER: US/10/361,460
PRIOR PILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 85
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 23
LENGTH: 1412
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54.0%;
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Best Local Similarity 66.9%;
Matches 236; Conservative
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Best Local Similarity 54.0
Matches 292; Conservative
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US-10-361-460-23
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ORGANISM: Zea mays
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              SEQ ID NO 1726
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APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21 (15401) B
CURRENT APPLICATION NUMBER: US/09/878,574
PRIOR PAPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
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APPLICANT: Byrum, Joseph R.
APPLICANT: Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21 (1540.18)
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT PILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILE APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
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GTGGAAAATTTGTCAGGAAGCAACATTTGACATTTGTTGGTGGGGACATGTTTAAATGC 754
                                                                          186 GTAGAGAACTTGACAGGGACCAATAATTTGAGTTTTTGTTGGTGGTGACATGTTCAACTCT 245
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Best Local Similarity 72.1%; Pred. No. 1.5e-28;
Matches 186; Conservative 0; Mismatches 72; Indels 0;
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ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 701097131H1
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; Patent No. US20020110548A1
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                                                   187 AATTITIGATTIGCCCCATGICATIGAAGAIGCCCCCATCTIAICCAGGAGIGGAACAIGTT
                                                                                                             GGTGGGGACATGTTTAAATGCATCCCCAAGGCTGATGCAGTTCTGCTTAAGTTGGTTTTA
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GTGTTGGAACGTCCAAATGTTGTGGAAAATTTGTCAGGAAGCAACAATTTGACATTTGTT
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APPLICANT: Bowen, Benjamin A.
APPLICANT: Bowen, Benjamin A.
APPLICANT: Bowen, Benjamin A.
TITLE OF INVENTION: Genes Encoding Enzymes for Ligmin
TITLE OF INVENTION: Biosynthesis and Uses Thereof
FILE REPREBRUCE: 0709
CURRENT APPLICATION NUMBER: US/10/361,460
CURRENT APPLICATION NUMBER: 60/057,082
FRIOR PELING DATE: 1997-08-27
NUMBER: OF SEQ ID NOS: 85
SOFTWARE: FRAELSEQ for Windows Version 3:0
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Publication No. US2003Q163839A1
GENERAL INFORMATION:
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Matches 290; Conservative
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US-10-361-460-24
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US-10-361-460-24
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LENGTH: 1315
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Fatent No. US20020110549A1

GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT APPLICATION NUMBER: US/09/878,574

CURRENT APPLICATION NUMBER: 09/33,535
FRICR FILING DATE: 1999-06-14
FRICR FILING DATE: 1999-06-14
SRICR FILING DATE: 1999-06-14
SRICR FILING DATE: 1999-06-14
SRICR FILING DATE: 1993-05-14
SRICR FILING DATE: 1997-06-14
SRICR FILING DATE: 1997-06-14
SRICR FILING DATE: 1997-06-14
SRICR FILING DATE: 1997-06-14
SRICR FILING DATE: 1997-06-14
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9.6%; Score 111.8; DB 10; Length 377;
Best Local Similarity 56.3%; Pred. No. 4.9e-20;
Matches 209; Conservative 0; Mismatches 162; Indels 0;
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; OTHER INFORMATION: Clone ID: LIB3028-009-Q1-B1-H12
US-09-878-574-3502
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US-09-878-574-3502
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Db 943 GATACTTGTTGGGATTCTTCCCGTGGCTCTGACAAAGGG 999 Qy 928 TGAACTAAAGCTCTTATGAATGATGCATGTTATTAATGGAAAAGAGAAA 987 Db 1000AGTCGTGATGATGATGTTGTTGTGGGGCGCACACCCCGGTGGAAAAGAGACA 1056 Qy 988 AGAAAAAGATTGAAGAAAACTTCATGGAAGCACACCCCGGTGGAAAATATCTCC 1047 Db 1057 CGAGAAGAATTTGAGCAAGCAAGCTGCTAAAGGTTTTGAAATATCTCC 1047 Db 1058 CTCACAGGATATTGATCTTTATGAAACT 1078 Db 1117 CTGTGCATTCAACACATGTCATTGAATTC 1107 Db 1117 CTGTGCATTCAACACACATGTCATTGAATTC 1177	RESULT 8 US-10-091-009-5 US-10-091-009-5 US-10-091-009-5 US-10-091-009-6 US-10-091-009-6 US-10-091-009-6 US-10-091-009-7 US-10-091-009-7 US-10-091-009-7 US-10-091-009-7 US-10-091-009-7 US-10-091-009-7 US-10-091-009-7 US-10-091-009-7 US-10-091-009-7 US-10-091-009-7 US-10-091-091-091-091-091-091-091-091-091-	; FEATURE: ; NAMES/KEY: misc_feature ; OTHER INFORMATION: AldOMT; GenBank accession number: X62096 US-10-091-009-5	Ouery Match Best Local Similarity 49.6%; Pred. No. 3.8e-19; Matches 313; Conservative 0; Mismatches 312; Indels 6; Gaps	OY 448 ALLIAGGETCUCTIAGGEACACCITTUTGGGGACTTTATCAATAAAGACCCTGCATAAAA 507 Db 523 ATTTAACAAGGCCTATGGGATGACTTTGAATATCAAGGATCCAGGATCAA 582 OY 508 CAAGTCATTCAATGAGGCAATGCTTGTGATTCTCAGATTGAACTTGACGTTTAGAGG 567 Db 583 CAAGTCTTCAACAAGGGAATGTCTGACCACTCTACCATTACCATGAAGAAGATCTTGA 642	OY 568 TIGCAATIGGGTCTTIGAGGACTGGAATCCATIGIGGATGTIGGTGGAACTGGAAT 627	OY 628 CACAGCAAAGATTATCTGTGAGGCTTTTCCTAAGCTGAAATGGTGTTGGAACGTCC 687	OY 688 AAATGTTGTGGAAATTTGTCAGGAAGCAACAATTTGACATTTGTTGGTGGGGACATGTT 747	Oy 748 TAAAIGCATCCCCAAGGCIGAIGCAGTCIGCTTAAGTTGGTTTTACAIAATTGGAATGA 807	Oy 808 CAACGAITGCAIGAAGAIATTAGAAAATIGTAAAGAAGCTATTTCAGGTGAAAGCAAAAC 867
Db 979 ATAAACAGTCAAACATCAAGAGACACAAGTTATGTTGATTTGTATATGATGG 1038	RESULT 7 US-09-947-027-5 1 Sequence 5, Application US/09947027 1 Sequence 5, Application US/09947027 2 Sequence 5, Application US/09947027 2 Sequence 5, Application US/09947027 3 Patent No. US20020124281A1 3 GENERAL INFORMATION: APPLICANT: Chiang, Vincent Lee C. APPLICANT: Li, Laigeng TITLE OF INVENTION: CELLUOSE CONTENT IN PLANTS TITLE OF INVENTION: CELLUOSE CONTENT IN PLANTS TITLE OF INVENTION: CELLUOSE CONTENT IN PLANTS CURRENT APPLICATION NUMBER: US/09/947,027 CURRENT APPLICATION NUMBER: US/09/947,027 CURRENT FILING DATE: 2000-09-05 PRIOR FILING DATE: 2000-09-05 NUMBER OF SEQ ID NOS: 14 SOFTWARRE: PatentIn version 3.0 SEQ ID NO 5 LENCTH: 1503 TYPE: DAA ORGANISM: aspen populus tremuloides NAMEKEY: misc feature OTHER INFORMATION: AldOMT; GenBank accession number: X62096 US-09-947-027-5	Query Match Query Match Best Local Similarity 49.6%; Pred. No. 3.8e-19; Matches 313; Conservative 0; Mismatches 312; Indels 6; Gaps 1;	OY 448 ATTTGAGGTCTCCTTAGGAACACCTTTCTGGGACTTTATCAATAAAGACCCTGCATATAA 507		628	OY 688 AATGTTGTGGAAAATTTGTCAGGAACAACAATTTGACAITTTGTTGGGGACAIGIT 747 Db 763 CCACGTCAITGAGGAIGCCCCAICTTAICCCGGAGIGGAGCAIGTTGGTGGCGACAIGIT 822	Oy 748 TAAATGCAICCCCAAGGCTGAIGCAGTTCIGCTTAAGTIGGAITGA 807 Db 823 IGTIAGTGIGCCCAAAGCAGATGCCGTTITCAIGAATGGAATG		, OY 868 AGGAAAAGTAGTTGTCATAGATACTGTGATAAAGGAAAAAAAA

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Sequence 13211, Application US/09878574
Batent No. US20020110548A1
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thomson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with TITLE OF INVENTION: Plants
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                                    APPLICANT: Kipp, Peter B.
APPLICANT: Kumar, Ramesh
APPLICANT: Kumar, Ramesh
APPLICANT: May, Gregory D.
TITLE OF INVENTION: The Use of Mixed Duplex Oligonucleotides
TITLE OF INVENTION: to Effect Localized Genetic Changes in Plants
TITLE OF INVENTION: TO Effect Localized Genetic Changes in Plants
CURRENT APPLICATION NAMBER: US/09/129,298
CURRENT FILING DATE: 1998-08-05
ERALIER FILING DATE: 1997-08-05
NUMBER: OF SEQ ID NOS: 19
SOFTWARE: FASTSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 52.6
Matches 259; Conservative
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LOCATION: (84)...(1178)
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Ta Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT APPLICATION NUMBER: 09/333,535
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR PILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
LENGTH: 279
                                                                                                                                                                                                                                                                1000 ---AGTCGTGCACGTTGATGTCATCCTGGCGCACACACCCCGGTGGGAAAGAGGAGGAC 1056
                                                                                                                                                                                                                                                                                                                         988 AGAAGAAGAITGGAAGAAACTCTTCATGGAAGCAGGGTTCCAAAAGCTACAAAATATCTCC 1047
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883 GGCCACTGCTTAAAATTCTTGAAGAATTGCTATGACGCGTTGCCGGAAAACGGCAAGGT 942
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CTHER INFORMATION: Clone ID: 701063901H1
US-09-878-574-10987
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Patent No. US20020110548A1
GENERAL INFORMATION:
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Publication No. US20030196218A1
GENERAL INFORMATION:
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                                                                                   ACCGTGGAATGTCTGATCACTCCACTATGTCAATGAAGAAGATTCTTGAGGACTACAAAG
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APPLICANT: Bowen, Benjamin A.
APPLICANT: Bowen, Benjamin A.
TITLE OF INVENTION: Genes Encoding Enzymes for Lignin
TITLE OF INVENTION: Biosynthesis and Uses Thereof
FILE REPREBRICE: 0709
CURRENT APPLICATION NUMBER: US/10/361,460
CURRENT APPLICATION NUMBER: 60/057,082
PRIOR PRILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 85
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 2.3e-18;
0; Mismatches 256;
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Best Local Similarity 51.3%;
Matches 273; Conservative
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; LOCATION: (57)...(1154)
US-10-361-460-25
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US-10-361-460-25
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LENGTH: 1306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 ACATAATCCACAGCCATAGCCATGGCCAACCCATTACTTTTTCAGAGTTGGTGTCAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 TACAAGTCCCACCAACTAAAACTCGTCAGGTGCAGAGCCTCATGCGTTATCTAGCACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cchargeaargacatrrdagiaccargecacagarccaagaircaagacaagarcca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Arnteen, Charles
APPLICANT: Arnteen, Charles
APPLICANT: Kipp, Peter B.
APPLICANT: Kumar, Ramesh
APPLICANT: May, Gregory D.
TITLE OF INVENTION: The Use of Mixed Duplex Oligonucleotides
TITLE OF INVENTION: to Effect Localized Genetic Changes in Plants
FILE REPERENCE: 7991-023-99
CURRENT APPLICATION NUMBER: US/09/129,298
CURRENT FILING DATE: 1998-08-05
EARLIER APPLICATION NUMBER: 60/054,386
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 12; Length 1418;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 107.6; DB 10;
Pred. No. 5.6e-19;
0; Mismatches 79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATTAAACAATGGCCGTAAAGCAAGTGAGATTT
FILE REFERENCE; 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 13211
LENGTH: 272
                                                                                                                                                                                                                                                                        TYPE: DNA
CRGANISM: Glycine max
CTHER INFORMATION: Clone ID: 701066773H1
US-09-878-574-13211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09129298
Publication No. US20030196218A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 ATGGATTCTTTGAGAT 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGGAATCTTTGAGAT 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 66.8 Matches 171; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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NAME/KEY: CDS
TATION: (59)...(1153)
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Best Local Similarity
Matches 231; Conserv
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US-09-129-298-4
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813 ATTGCATGAAGATATTAGAAAATTGTAAAGCTATTTTCAGGTGAAAGCAAAACAGGAA 872
                                                                                   854 ATTGCATAAAGATATTGAAGAATTGCAAAGAAGCGGTCCCTCCAAATATCGGAAAAGTGT 913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              607 GGAATGTCCAATCATTCGACCATTACCATGAAGAAAATCCTTGAGACTTACAAAGGGTTC 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGGACTIGGATCTGTGGTIGATGTTGGTGGCACTGGTGCCCACCTTAACATGATT 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATATTAGAAAATTGTAAAGAAGCTATTTCAGGTGAAAGCAAAACAGGAAAAGTAGTTGTC 883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              464 GGAACACCTTTCTGGGACTTTATCAATAAAGACCCTGCATATAACAAGTCATTCAATGAG
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                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/09796256A

Patent No. US20020078477A1

GENERAL INFORMATION:
APPLICANT: Chiang, Vincent L
APPLICANT: Carraway, Daniel T
APPLICANT: Smeltzer, Richard H
ITILE OF INVENTION: Production of Syringyl Lignin in Gymnosperms
ITILE OF INVENTION: Production of Syringyl Lignin in Gymnosperms
ITILE REFERENCE: 50617/c-2382.0

CURRENT APPLICATION NUMBER: US/09/796,256A

CURRENT APPLICATION NUMBER: US60/03381

PRIOR PILING DATE: 1996-12-16

PRIOR PILING DATE: 1996-12-16

PRIOR FILING DATE: 1997-12-12

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PatentIn Ver. 2.1
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Pred. No. 4.9e-15;
0; Mismatches 309;
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ORGANISM: Liquidambar styraciflua
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ilarity 50.1%;
Conservative (
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; LOCATION: (67)..(1170)
US-09-796-256A-5
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Best Local Similarity
Matches 325; Conserv
                                                                                                                                  873 AAGTAGTTG
                                                                                                                                                                                                                                                          RESULT 15
US-09-796-256A-5
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Sequence 2582, Application US/09938842A

Patent No. US2002016037841

GARBEAL INFORMATION:
APPLICANT: Marper, Jeff

APPLICANT: Marper, Joef

APPLICANT: Maryo, Xun

APPLICANT: Maryo, Xun

APPLICANT: ALM, Tong

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

FILE REFERENCE: SCRIP1300-3

CURRENT APPLICATION NUMBER: US/09/938,842A

CURRENT APPLICATION NUMBER: US 60/227,866

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR FILING DATE: 2001-08-24

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

SEQ ID NO 2582

LENGTH: 1149
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                                                                                                                                                         936
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TCCACCTGCAACCGCCGTTTTCTTCAAGACAACTCTATGTGACTGGGGTGACGACGAGTG 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      613
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                                                                                                                                                                                                                                                                                                                                                                                            674 IGGGGAIGCITGTGAAGGAGITICCITGGAICAAAGGATITAACITIGATCTICCICAIG
                                                                                                                                                    877 AGTIGICATAGATACIGIGATAAACGAAAACAAAGAIGAGCGCCAAGTIACIGAACIAAA
                                                                                                                                                                                                                                                                                                   .010 AGTTATGTTTGATTTGGTTATGATGGCGG---TCAATGGAGTCGAGCGAGCAAGA
                                                                                                                                                                                                                                                                                                                                                     997 ITGGAAGAAACICITCAIGGAAGCAGGGITCCAAAGCIACAAAAIAICICCCITCACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 516 TCAATGAGGCAATGGCTTGTGATTC---TCAGATGTTGAACTTGGCGTTTAGAGATTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                554 rchardaddchiddedrichidaddadddaddddaddchadcaddadchidrc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  573 ATTGGGTCTTTGAGGGACTGGAATCCATTGTGGATGTTGGTGGTGGAACTGGAATCACAG
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0; Mismatches 158; Indels
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Matches 208; Conservative
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884 ATAGATACTGTGATAAGGAAAAGATGAGGGGGCGAAGTTAGTGAAGTAAAGGTCGTT 943
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456.2 39.3 42.5 494 9 AL507864 456.2 39.3 852 10 BG588377 442.6 38.2 82.10 BG588377 437.9 569 12 BM188258 437.4 37.7 606 12 BM177364 417.8 36.0 788 13 BQ165419 415.8 35.8 693 14 GM21971 441 35.6 546 12 BM178815 410 35.6 546 12 BM178815 410 35.6 546 12 BM178815 410 35.6 546 12 BM178815 410 35.6 546 12 BM178815	405 34.9 775 3 80165420 397.2 34.9 775 3 80165420 390.6 33.7 742 9 AW567810 387 33.4 408 13 8075689 385.8 33.3 503 10 BG511336 383.2 33.0 420 10 BG511336 375.8 32.4 512 10 BG505454 364 31.4 551 9 AW309379	353.8 30.5 519 10 BG509170 348.8 30.1 668 13 BQ156708 348.8 20.1 746 13 BQ156708 330.8 29.1 563 12 BM528698 330.2 28.5 763 9 AW348354 327.2 28.2 519 10 BF648180 327.2 28.2 519 10 BF648180 327.2 28.2 519 10 BF648180	320.8 27.7 592 13 BU577747 BU577747 Sar92a10. 318 27.4 634 10 BR65039 BU577747 Sar92a10. 310.4 26,8 779 14 CB91286 CB91286 CB91286 EST640255 309.6 26.7 496 13 BU549771 GM8800238 BU549771 GM8800238 BU549771 GM8800238 BU549771 GM8800238 S2.4 615 10 BG448331 BG448331 BG448331 BG448331 BG448331 BG448331 BG448331 BG47747 Sar93G06. 287.4 24.8 577 9 AW559532 AW559532 BST34580 AW559532 BST34580 S285.4 24.5 577 9 AW559532 BST3458 AW559532 BST34580 S285.4 24.5 577 9 AW559534 AW559532 BST3458 S288 S248 S248 S248 S248 S248 S248 S24	1 90/c TION GW1210008410D3 Gm-r1021 Glycine max cDNA clone Gm-r1021-2837 3', ION AW350290.1 G1:6848000 NA AW350290.1 G1:6848000	Glycine max (soybean) Glycine max Glycine max Eukaryota, Viridiplantae, Streptop Spermatophyta, Magnoliophyta, eudi reurosids I; Fabales; Fabaceae; F Glycine. 1 Glycine. 1 Vodkin, L., Keim, P., Shoemaker, R., Erpelding, J., Reph, C., Shoemaker, R., Freelding, J., Reph, C., Shoop, E., P.	A Functional Genomics Figgram for Soybean (NSF 986 Unpublished Other_ESTS: A1507864 Other_ESTS: A1507864 Soybean (NSF 9872565) Lewin, H. A., Director, Keck Center for Comparative Genomics University of Illinois Edwin R. Madigan Building, 1201 W. Gregory, Urbana Tel: (217) 244-6147
0 14444 14444	C 221		Ω ω ω ω ω ω α α α α α α α ω α α α α α α α	RESULT 1 AW350290/C LOCUS . DEFINITION ACCESSION VERSION KEYWORDS	SOURCE ORGANISM REFERENCE AUTHORS	COMMENT
n 5.1.6 Compugen Ltd. , Search time 2914 Seconds (without alignments) (without alignments)	gtt	ers: 45562784			results predicted by chance to have a to the score of the result being printed, of the total score distribution.	Description AW350290 GM210008A BM523459 sam64a09, BQ452916 sac93b08. B1245401 F1SIC9 Fo
GenCore version 5 Copyright (c) 1993 - 2003 Cc nucleic search, using sw model November 9, 2003, 23:36:19; 6 (wi)	US-09-868-547-3 1160 1 gtttgctattatggcttctt IDENTITY NUC Gapop 10.0 , Gapext 1.0 22781392 seqs, 12152238056 resi	f hits satisfying chosen parameters: length: 0 length: 200000000 Maximum Match 0%	EST:* 1: em_estba:* 2: em_estlum:* 4: em_estlum:* 5: em_estlum:* 6: em_estlu:* 7: em_estlu:* 7: em_estlu:* 11: qb_hc:* 11: qb_hc:* 11: qb_hc:* 13: qb_est1:* 13: qb_est1:* 13: qb_est1:* 13: qb_est1:* 14: qb_hc:* 15: qb_est1:* 16: qb_hc:* 17: qb_est1:* 18: qb_hc:* 18: qb_hc:*		em_gss_rod:* em_gss_phg:* gp_gssI:* gb_gss2:* gb_gss2:* the number of than or equal	\$Udery Autch Length DB ID 56.9 697 9 AW350290 50.7 589 12 BM522459 48.1 561 13 BQ452916 47.2 573 12 BI245401

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                                 This clone is available through: Genome Systems, Inc. 4633 World parkway Circle St. Louis, Missouri 63194. For further information call: (800) 430-0030 or (314) 427-3222 PAX:(888)919-3334 or (314) 427-3324 or contact:clones@genomesystems.com or info@genome
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157 c 97 g 221 t 24 others
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Seq primer: 5'-TTTTTTTTTTTTTT(A/C/G)-3'.
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589 bp mRNA linear EST 19-FEB-2002 gm-c1087-000 Gm-c1087-426 5' similar to TR:022555 022555 O-METHYTRANSPERASE. [2] TR:022308 ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@warson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-53-4363 or contact: ccu@resgen.com web site:
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/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
Xhol; The mRNA was prepared using polyafract mRNA system
from PROMEGA. The cDNA was prepared using the STRATAGENE
Kit. Complementary DNA was synthesized from mRNA using a
primer consisting of a poly(dT) sequence with a Xhol
                                                                                                                                                                                                                                                              985 AAAAGAAGAAGATTGGAAGAARCTCTTCATGGAAGCAGGGTTCCAAAGCTACAAAATATC 1044
                                                                                                                                                                                              159
924
                                                               278 AACAGGAAAAGTAGTTGTCATAGATACTGTGATAAACGAAAACAAAGATGAGGCGCCAAGT 219
                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 TCCCTTCACAGGATALTTGICTCTTALTGAGATCTATCCTTGAATACTGACGCTGCAATA 39
                                                                                                                               925 TACTGAACTAAAGCTCCTTATGGATGTACACATGGCATGTATTATTAATGGAAAAGAGAG
                                                                                                                                                                                              218 TACTGAACTAAAGCTCCTTATGGATGTACACATGGCATGTATTATTAATGGAAAAGAGAG
865 AACAGGAAAAGTAGTTGTCATAGATACTGTGATAAACGAAAACAAAGATGAGCGCCAAGT
                                                                                                                                                                                                                                                                                                                          158 AAAAGAAGATTGGAAGAACTCTTCATGGAAGCAGGGTTCCAAAGCTACAAATATC
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Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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/db_xref="taxon:3847"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 TTCCATTTAGTAGTTAATTTGCATGTTATCAATAAAT 1
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High quality sequence stop: 438.
Location/Qualifiers
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/lab_host="DH10B"
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Fax: 314 286 1810
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Fax: 314 286 1800
Email: estewatson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
              Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       565 AGATTGCAATTGGGTCTTTGAGGGACTGGAATCCATTGTGGATGTTGGTGGTGGAACTGG
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/db_xref="taxon:3847"
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/lab_host="DH108"
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Public Soybean EST Project
Washington University School of Medicine
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                               EcoRI adapters (5'OH-AATTCGGCAGGA and 3'GCGTGCTCP) were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction sites of the pBluescript vector. The vector was previously dephosphorylated. The ligated cDNA fragments were transformed into DH10B by electroporation. Library is in LB medium with ampicillin and glyverols. A verage insert size: 800 bp."
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EST.
Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Pred. No. 1.8e-117;
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                                 /note=Torgan: Root: Vector: pGEM; Forrest roots were inoculated with Fusarium solani f. sp. glycinae and samples were collected after 14 days of inoculation. Total RNA was used for CDNA synthesis using SMART PCR CDNA synthesis kit (CLONTECH, CA). CLONTECH PCR. Select Subtraction system was used to enrich rare transcripts expressed in Forrest roots under inoculation by F. solani and cloned in pGEM vector. ESTS were sequenced using M13 universal forward or reverse primer."
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sa88bd.yl Gm-c1004 Glycine max cDNA clone GRNOWE SYSTEMS CLONE ID: GGm-c1004-6344 5' similar to TR:022308 022308 7-0-METHYLTRANSFERASE.
[3] TR:022309 TR:022555 ;, mRNA sequence.
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; rosids
i_eurosids I; Fabales, Fabaceae, Papilionoideae, Phaseoleae,
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Idbal,M.J. and Lightfoot,D.A.
Differentially expressed mRNA sequences identified by subtraction hybridization from soybean, Glycine max (L.) Merr. var. Forrest, roots in response to Fusarium solani f. sp. glycinae inoculation Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Igbal MJ and Lightfoot, DA Center of Excellence in Soybean Research, Teaching and Outreach Southern Illinois University at Carbondale Room 176, Ag. Building, Mail Code 4415, Carbondale, IL 62901-4415,
AATCACAGCAAAGATTATCTGTGAGGCTTTTCCTAAGCTGAAATGCATGGTGTTGGAACG
                              TGACAACGATTGCATGAAGATATTAGAAAATTGTAAAGAAGCTATTTCAGGTGAAAGCAA
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                                                                                                     TCCAAATGTTGTGGAAATTTGTCAGGAAGCAACAATTTGACATTTGTTGGTGGGGACAT
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/cultivar="Forrest"
/db_xref="taxon:3847"
/dev_stage="14 days after inoculation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 618 453-3121
Fax: 618 453-7457
Email: mjiqbal@siu.edu, ga4082@siu.edu
Seg primer: M13 Forward.
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TITLE
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KEYWORDS
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251

191

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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Medicago.

1 (bases 1 to 852)

Harrison, M.J., Liu, J., Town, C.D., Van Aken, S., Utterback, T., Cho, J.

and Fraser, C.M.

ESTs from phosphate-starved roots of Medicago truncatula, 2001
Unpublished
Contact: Harrison M.J.
Contact: Harrison M.J.
Contact: Harrison M.J.
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mjharrison@noble.org
The Samuel Roberts Noble Foundation: N387128e TIGR sequence name:
MTHAY18TK More information is available at: http://www.medicago.org
Seq primer: SKmod (CTA gard grg gAT CC).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 12-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 TCACTGCTGCTTCAGAGTTACTTGTCAAAAGAGTGAGCTTAGTTTAGCTCCAATGGTTG 360
                                                                                                                                                                                                                                                                                                                         TAGCACACAATGGATTCTTTGAGATAGTAAGAATCCATGACAACATAGAAGCATATGCTC 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                372 AGTATTTTCTTGAACCAAATTGTCAAGGTGCATGGAACCAGTTGAAGAGGTGGGTTCATG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 AGTATITICITGAACCAAATIGICAAGGIGCAIGGAACCAGITGAAGAGGIGGGITCAIG 420
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EST490186 MHRP- Medicago truncatula cDNA clone pMHRP-53C11, mRNA
        121 ACATACCCGACATAATCCACACATAGCCATGGCCAACCCATTACTTTTCAGAGTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                     TCACTGCTGCTTCAGAGTTACTTGTCAAAAGCAGTGAGCTTAGTTTAGCTCCAATGGTTG
                                                                                                           TTCAGAGTTGG
                                                                                                                                                                                                           TGTCAATTCTACAAGTCCCACCAACTAAAACTCGTCAGGTGCAGAGCCTCATGCGTTATC
                                                                                                                                                                                                                                                                  TGTCAATTCTACAAGTCCCACCAACTAAAACTCGTCAGGTGCAGAGCCTCATGCGTTATC
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/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               432 AGGAAGATCTCACAGTATTTGAGGTCTCCTTAGGAACACCTTTCTGGGACTTTATCAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Medicago truncatula (barrel medic)
Medicago truncatula
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheo;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                  ACATACCCGACATAATCCACAGCCATAGCCATGGCCAACCCATTACTTT

    852
/organism="Medicago truncatula"
/oul_type="MRNA"
/oul_tyar="A17"

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/lab_host="XLOLR"
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/clone="pMHRP-53C11"
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Fax: 580-221-7380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strategene's first-strand synthesis primer was used Strategene's first-strand synthesis, the CDNA ends were 'polished' with clone Fitu DNA polymerase, ligated to EcoRI adapters, and phosphorylated. The XhoI site within the first-strand synthesis primer was restricted by digestion with XhoI; all XhoI sites in the CDNA would be protected by their hemimethylated status. The CDNA constructs were size-fractionated with a Soubp cutoff, using GibcoBRI Life Fechnologies' CDNA Size Fractionation column. The column eluent was then ligated into Stratagene's pBluescript II XR Predigested vector (pBluescript II SK(+) that had been digested with EcoRI and XhoI, and phosphorylated). Both the white and blue colonies appear to contain recombinant plasmids with CDNA inserts. Blue colonies 9n=15) have been sequenced, and possess putative CDNA inserts. This library was constructed by Doy. Paul Keim & Virginia H. Coryell, Department of Biology, BoxS640, Northern Arizona University, Flagstaff, AZ 86011, Phone: 520-523-1078 (Dr. Pull, Reim, Coryell), email: paul Keim, coryell@nau.edu, virginia.coryell@nau.edu.
                 Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, P., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1800
Exa: 314 286 1800
Exa: 314 286 1800
Exa: 314 286 1800
Exa: 314 286 1800
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 1307 5td Exror: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue type="root"
/lab host="XL10-Gold"
/clone_lib="Gam-clood"
/clone_lib="Gam-clood"
/note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2:
XhoI; Root cDNA. The mRNA was isolated from entire roots
of 8 day old 'Williams' seedlings which were propagated on
paper towels with distilled water. Stratagene's CDNA
Synthesis Kit (catalog #200401) was used to synthesis the
CDNA. First- strand synthesis was performed with 5-methyl
dCTP, hence the ligated CDNA is hemimethylated.
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                                                                                                                                                                                                                      Unpublished
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="GENOME SYSTEMS CLONE ID: Gm-c1004-6344"
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Pred. No. 8.1e-97;
0; Mismatches 1; Indels
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Seg primer: -40RP from Gibco
High quality sequence stop: 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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(bases 1 to $94)
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source

FEATURES

Query Match Best Local S Matches 493

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BASE COUNT

ORIGIN

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Medicago truncatula
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids
; eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae,
                                                                                                    822 bp mRNA linear · EST 24-APR-2001 KV3 Medicago truncatula cDNA clone pKV3-46C11 5' end,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAACATGTATGCTTTCATAGATTCCATGTCTTTAAATGGTCAGTTGAAATGGACATAC 134
                                                                                                                                                                                                                                                                                                                                                                                        Town, C.D., Bowman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /moi_type="mRNA""
/cultivar="gencype A17"
/dultivar="gencype A17"
/db xef="lexxon:3880"
/clone="pKV3-46C11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     189 ITCTTCAAATTCCATCAACCAAAGTCGATAACGTGCAGCGTCTCATGCGTCTCCTTGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCGACATAATCCACAGCCATAGCCATGGCCAACCCATTACTTTTCAGAGTTGGTGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAACTATTATCTAC-----AATCATGGCAAACCAATTACTCTTTCAAACTTAGTTTCAA
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ESTs from roots of Medicago truncatula 72 h after Rhizobium inoculation, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
Contact: VandenBosch K
Department of Plant Biology
University of Minnesota
220 BioSci Center, 1445 Gortner Ave, St. Paul, MN 55108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M393775E TIGR Sequence name: MTECA18TK More information available at: www.medicago.org Seq primer: SKmod (CTA gAA CTA gtg gAT CC). Location/Qualifiers
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    .822
/organism="Medicago truncatula"

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                                                                                                                                                                                                                                Medicago truncatula (barrel medic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kvandenb@cbs.umn.edu
                                                                                                                                                                                     BG645368.1 GI:13780480
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Fax: 612 625 1738
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XhoI; At the trifoliate stage, M. truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this period, they were fertilized twice weekly with 1/2 Hoaglands solutions containing 20um potassium phosphate. cDNA was prepared from polyA+ enriched RNA. The CDNA was directionally ligated into the Unizap XR vector from Strateagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing phase using Ex-assist helper phage and propagated in
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                                                                                                                                                                                                                                                                                                                 DB 10; Length 852;
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South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact: ccu@resgen.com web site: Seq primer: -40RP from Gibco High quality sequence stop: 425.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pBlusscript vector. The ligated cDNA fragments were transformed into E.coli ElectroMax DH10B host cells. Plant care, inoculations, and library construction were performed by Steve Clough (Lila Vodkin lab, University of Illinois)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 MAGICAAAAGCAGTGAGCTTAAGTTTAGCTCCAATGGTTGAGTATATTCTTGACACAACTA 177
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                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="hason:1847"
/clone="SOYBRAN CLONE ID: Gm-c1074-4849"
/tissue_type="seedlings induced for HR (hypersensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 caddraaagrraardaaagrachaagrachaagagrraagaardaaragarrarra
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37.9%; Score 439.2; DB 12; Length
Best Local Similarity 86.7%; Pred. No. 4.2e-85;
Matches 496; Conservative 0; Mismatches 73; Indels
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
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1 (bases 1 to 569)

2 (boses 1 to 569)

3 (boemaer, R. Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin, T., Jackson,Y., Cardenas,M., McCann,Public Soybean EST Project
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4444 Forest Park Parkway, Box 8501, St. Louis, MO
Fax: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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Public Soybean EST Project
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consisting of a poly(dT) sequence with an XhoI restriction site. EcoRI adaptors were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The CDNA insert is protected from KhoI digestion via methylation during first strand synthesis. The CDNA fragments were directionally closed into the EcoRT-XhoI restriction site of the PBJURESCRIPT restriction site of the transformed into E.coli ElectroMax DHIOB host cells. Plant care, inoculations, and library construction were performed by Steve Clough (Lila Vodkin lab, University of Illinois).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                788 bp mRNA linear EST 25-APR-2002 truncatula cDNA clone pKVKC-9A5, mRNA
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Pred. No. 1.1e-84;
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Best Local Similarity 85.6
Matches 525; Conservative
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/lab_host="9-11 day old"
/lab_host="DH10B"
/clone_lbb=[dm-cl074"
/note="Wector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhO1; The CDNA library was constructed from mRNA isolated
from 9-11 day old seedlings that were induced for HR
(hypersensitive response) by vacuum infiltrating plant
tissue with Pseudomonas syringae pv. glycinea carrying the
avrB gene (Genetics 141:1597-1604). Plant tissue (expanded
unifoliate leaves) was collected at 2, 4, 8, 12, 24, 36,
and 53 hrs after inoculation and their mRNA pooled equally
for cDNA construction. The library was prepared using the
Stratagene pBluescript II SK(+) library construction kit.
Complementary DNA was synthesized from mRNA using a primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
www.resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BM177364 606 bp mRNA linear BST 06-DEC-2001 saj80d09.y1 Gm-c1074 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1074-2873 5' similar to TR:022555 022555 O-METHYTRANSFERASE. [2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids
eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,
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                                                                           CCAAGATTATCTGTAAGCATTTCCTGACTTGAAATGCATTGTGTTTGACCGTCCGCAGG
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                            CAAAGATTATCTGTGAGGCTTTTCCTAAGCTGAAATGCATGGTGTTGGAACGTCCAAATG
                                                                                                                                                 TTGTGGAAAATTTGTCAGGAAGCAACAATTTGACATTTGTTGGTGGGGACATGTTTAAAT
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High quality sequence stop: 4
Location/Qualifiers
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BM177364.1 GI:17400582
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Glycine max
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EST 09-MAY-2003
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/note="Vector: pBluescript SK-; Site_l: EcoRI; Site_2:
Xhol; cDNA was prepared from polyA+ enriched RNA. The cDNA
                           512
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosid,
eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
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VandenBosch, K., Endre, G., Silverstein, K, Town, C.D., Van Aken, S., Utterback, T., Cheung, F. and Fraser, C.M.
The Medicago truncatula 6K unigene set: cDNA clones selected and re-arrayed from various libraries
                                                                                                                                                    CATICAATGAGGCAATGGCTTGTGATTCTCAGATGTTGAACTTGGCGTTTAGAGATTGCA
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                    AGGICTCCTIAGGAACACCTTICTGGGACTTTATCAATAAAGACCCTGCATATAACAAGT
                                                                                      GTGTTACTTTAGGGTCTGGTTTTTGGGATTTTTCTTGATAAAATCCTGAATATAAAAGAT
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EST639689 MTUS Medicago truncatula cDNA clone MTUS-46H12, mRNA
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University of Minnesota
220 BioSci Center, 1445 Gortner Ave, St. Paul, MN 5510
Tel: 612 624 2755
Fax: 612 625 1738
Email: kvandenbecbs.umn.edu
Alias Clone DSIR-19116
TIGR sequence name: MTUBT96TV
More information is available at: www.medicago.org
Seq primer: (gtA AtA CgA CtC Act AtA ggg C).
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/cultivar="A17"
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/dev_stage="various stages"
/lab_host="XLOLR"
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/clone="MTUS-46H12"
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Contact: VandenBosch
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/clone_lib="KVKC"...
/clone_lib="KVKC"...
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
Xhoi; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."

a 119 c 166 g 276 t
                                     Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                                                                                                                     (Dases 1 to 788)
VandenBosch, K., Endre, G., Silverstein, K., Town, C.D., Van Aken, S., Utterback, T., Cheung, F. and Fraser, C.M.
The Medicago truncatula 'kiloclone' set; ESTs selected and re-arrayed from various libraries
Unpublished
                                                                                                                                                                                                                                                                                                                                Contact: VandenBosch K
Contact: VandenBosch K
Department of Plant Biology
University of Minnesota
220 BioSci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
Tel: 612 612 775
Fax: 612 629 175
Bmail: kvandenb@cbs.umn.edu
TIGR sequence name: MTMAIO5TK Alias Clone name:DSIR-19116 More
information is available at: www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
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/mol_type="mRNA"
/cultivar="A17"
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/lab_host="XLOLR"
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/clone="pKVKC-9A5"
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/dome_liber_Gmccl072"
//note=Tubsc=Cnlubs.
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//note=Tubsc=Cnlubs.
//note=Tubsc=Cnlubs.
//note=Tubscalon library was constructed from mRNA isolated from xhoi; The CDNA library was constructed from mRNA isolated from 2-3 week old seedlings that were induced for symptoms of SDS (Sudden Death Syndrome) disease by the translocation of culture filtrate of Fusarium solani f. Sp. glycines (Plant Cell Report 18:375-380). Cultivar PI 567374 is partially resistant to the disease SDS. Plant tissue (expanded leaves, folded leaves, and new shoots) were collected at 1, 6, 24, and 48 hrs. after inculation and their mRNA pooled equally for CDNA construction. The library was prepared using the Stratagene pBluescript II SK(+) library was prepared using the Stratagene pBluescript II SK(+) library was prepared using the Stratagene pBluescript II sapports were ligated to the blunt-ended CDNA fragments apply(dT) sequence with an XhoI restriction site. BcoRI adaptors were ligated to the blunt-ended CDNA fragments followed by XhoI digestion. The CDNA inscribed conditionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into B.coll ElectroMax DHIOB host cells. Plants were inoculated by Shuxian Li (Glen Hartman lab, University of Illinois). Library was constructed by Steve Clough (Lila Vodkin lab, University of Illinois).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
                                                                                          1 (Dases 1 to 546)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,R., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Sohurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 ATTACTITITICAGAGTIGGIGTCAATTICTACAAGTCCCACCAACTAAAACTCGTCAGGTG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGAGCCTCATGCGTTATCTAGCACACAATGGATTCTTTGAGATAGTAAGAATCCTGAC 292
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                        eudicots;
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                      ophyta; eudicotyledons; core eudicots;
Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  οĘ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1072-4190"
/clasue type="seedlings induced for symptoms (Sudden Death Syndrome) disease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 546;
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                                                                                                                                                                                                                                                                                                                                  Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 413; DB 12;
Pred. No. 2.1e-79;
                                                                                                                                                                                                                                                                                                                                                                                                               4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 t
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="2-3 weeks old"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               www.resgen.com
Seg primer: -40RP from Gibco
High quality sequence stop: 421.
Location/Qualifiers
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/organism="Glycine max"
                   Spermatophyta; Magnoliophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
                                              eurosids I; Fabales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
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ses 471; Conservative
                                                                       Glycine
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1074 AGAICTATCCTTGAATACTGACGCTGCAATATTCCATTTAGTAGTTAATTTGCATGTTAT 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      saj59h07.yl Gm-c1072 Glycine max cDNA linear EST 06-DEC-2001 Gm-c1072-4190 5' similar to TR:022555 022555 0-METHYTRANSPERASE. [2] TR:022308 ;, mRNA sequence.
was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."
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BM178815.1 GI:17402033
BST.
Glycine max (soybean)
Glycine max
Elkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                  533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTGTAAAGAAGCTATTTCAGGTGAAAGCAAAACAGGAAAAGTAGTTGTCATAGATACTG 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         333 Aaridraakdaadcrorracaaaridaroddaaaaadddaacaardarraradariarod 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGATAAACGAAAAAGATGAGCGCCAAGTTACTGAACTAAAGCTCCTTATGGATGTAC 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCAATAATTTGACTTATGTTGGTGGGGACATGTTCACATCTATTCCTAATGCTGATGCAG 394
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                                                                                                                                                                                                                                                                                                                    TCTGGGACTTTATCAATAAAGACCCTGCATATAACAAGTCATTCAATGAGGCAATGGCTT
                                                                                                                                                                                                                                                                                                                                                                           TTTTGGATTTTCTTGATAAAATCCTGAATATAATAGATCATTTAATGATGCAATGGCTA
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ش
                                                                                                                                                                                                                         Length 693;
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                                                                                                                                                                                                                      DB 14;
                                                                                                                                                                                                                    Score 415.8; DB 1.
Pred. No. 5.4e-80;
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77.5%;
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                                                                                                                                                                                                                                            Local Simines 517;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36
                                                                                                                                 BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                  Watches
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/dev_stage="various stages"
/lab.host="XtOLR"
/clone_lib="KVKC"
/clone_lib="KVKC"
/note="Vector: pBluescript SK-; Site_l: EcoRI; Site_2:
Xhol; cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."
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                                                                                                                                                                                                                                                                                                                                  TITGCTATTATGGCTTCTTCATTAAACAATGGCCGTAAAGCAAGTGAGATTTTTCAAGGT
                                                                                                                                                                                                                                                                                                                                                                     29 TTTGCAGGTGTATGGGCTTCTTCAATAATAACCGTAAAGCAAGTGAAATTTTCAAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTGAGCTTGACATACCCGACATAATCCACAGCCATAGCCATGGCCAACCCATTACTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCAGAGITGGIGICAATICTACAAGICCCACCAACTAAAACTCGICAGGIGCAGAGCCIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAGAAGAAGCTTATGCTCTCACAGTTACTTCAGAGCTTCTTGTTAAAGGGACTGAACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      563 AGTGATTCCAAAATGATTAATTTTGGCATTGAAAGATTGCAATTTTGTGTTTTGAGGGGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAATCCATTGTGGATGTTGGTGGAACTGGAATCACAGCAAAGATTATCTGTGAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATTCAATTGTGGATGTTGGTGGAAATGGAACAACTGGTAAGATTATTTGTGAGACA
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University of Minnesota
220 BloSci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
Tel: 612 624 2755
Fax: 612 624 2755
Fax: 612 625 1738
Email: kvandenb@cbe.umn.edu
TIGR sequence name: MTNAI04TK Alias Clone name:DSIR-19C17 More
information is available at: www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
                                           AACATAGAAGCATATGCTCTCACTGCTTCAGAGTTACTTGTCAAAAGCAGTGAGCTT
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eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
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VandenBosch,K., Endre,G., Silverstein,K, Town,C.D., Var Utterback,T., Cheung,F. and Fasser,C.M.
The Medicago truncatula 'kiloclone' set; ESTs selected re-arrayed from various libraries
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Email: kvandenb@cbs.umn.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu.
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4353 or contact via email: ccu@resgen.com
Seg primer: -40RP from Gibco
High quality sequence stop: 411.
                                                                                                                                                                                                                                                                                                                                                                                              Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, Shoemaker, R., Keim, P., Vodkin, L., Kucaba, T., Martin, J., Beck, C., A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harrey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                   Bukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I, Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                      AW733746 625 bp mRNA linear EST 03-DEC-2001 sk77f10.yl Gm-c1016 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1016-10148 5' similar to TR:022309 022309 7-0-METHYLTRANSFERASE.;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    512 TCATTCAATGAGGCAATGGCTTGTGATTCTCAGATGTTGAACTTGGCGTTTAGAGATTGC 571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
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/dlone="GBNOME SYSTEMS CLONE ID: Gm-c1016-10148"
/laisue_type="immature flowers of field grown plants"
/lab host="XL10-Gold"
/clone_lib="Gm-c1016"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.9%; Score 405; DB 9; Length 625; ilarity 79.4%; Pred. No. 1.2e-77; Conservative 0; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
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101 c
                                                                                                                                                                                                                                                         Glycine max (soybean)
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Fax: 314 286 1810
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ORIGIN
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                                                                                                        DEFINITION
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VERSION
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                                 RESULT 14
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                                                      AW733746
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
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5/2 AATTGGGTCTTTGAGGGACTGGAATCCATTGTGGATGTTGGTGGTGGTAGTGGAACTGGAATCACA 631
                                                                                        125 AAGTTGGTGTTTGAGGGACTGGAATCCATTGTGGATGTTGGTGGTGGAACTGGAGCCACT 184
                                                                                                                                                                                 GCAAAGATTATCTGTGAGGCTTTTCCTAAGCTGAAATGCATGGTGTTGGAACGTCCAAAT 691
                                                                                                                                                                                                                                                                          185 GCCAGGATGATCTCTGAAGCATTTCCTGACTTGAAATGCGTTGTGCTTGACCGTCCTCAC 244
                                                                                                                                                                                                                                                                                                                                                                        GTTGTGGAAAATTTGTCAGGAAGCAACAATTTGACATTTGTTGGTGGGGACATGTTTAAA 751
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VandenBosch, K., Endre, G., Silverstein, K., Town, C.D., Van Aken, S., Utterback, T., Cheung, F. and Fraser, C.M.
The Medicago truncalla 'Kiloclone' set; ESTs selected and re-arrayed from various libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGR sequence name: WTNAIGSTV Alias Clone name:DSIR-19L16 More information is available at: www.medicago.org Seq primer: (gtA AtA CgA CtC ACt AtA ggg C).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  869 GGAAAAGTAGTTCATAGATACTGTGATAAACGAAAACAAAGATGAGCGCCAAGTTACT
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ST611277 KVKC Medicago truncatula cDNA clone pKVKC-9A5, mRNA
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Department of Plant Biology
University of Minnesota
220 Biosci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
Tel: 612 624 2755
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/db xref="taxon:3880"
/clone="pKVKC-9A5"
/tissue type="mixed tissues"
/tissue type="mixed tissues"
/dev_stage="various stages"
/lab_host="XLOLR"
/clone lib="KVKC"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using cigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."
72 a 158 c 90 g 255 t
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Pred, No. 1.2e-77;
0; Mismatches 145; Indels
cultivar="A17"
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 77.6%;
Matches 516; Conservative
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Search completed: November 10, 2003, 01:51:24 Job time : 2919 secs